U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office **SEARCH REQUEST FORM** Attain Poper #11 Requestor's Serial Brown Loen 09/715,249 Name: Number: Phone: 605-1197 Art Unit: ____ 1636 MATLBOX: 11 E12 OFFICE: Search Topic: Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s). Please seven the commercial merende 2034 SEGID No. 1 Edward Hart Technical Info Specialist STIC / Biotech CMI 12C14 Tel: 305-9203 STAFF USE ONLY Search Site Terminal time: STN Elapsed time: Dialog CPU time:____ Type of Search APS N.A. Sequence Total time: Geninfo Number of Searches: A.A. Sequence SDC DARC/Questel Number of Databases: Structure Bibliographic Other

Database: GenEmbl:* 1	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	.1 number of hits satisfying chosen parameters: 2944280	Searched: 1472140 seqs, 8248589755 residues	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Title: US-09-715-249-1_COPY_1_2034 Perfect score: 2034 Sequence: 1 atgcgaccctccgggacggcacatcgttcggaagcgcacg 2034	Run on: January 14, 2002, 19:04:15; Search time 2222.52 Seconds (without alignments) 15097.845 Million cell updates/sec	OM nucleic - nucleic search, using sw model	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10	RESULT 1 AX179384 LOCUS DEFINITION ACCESSION VERSION KEYWORDS		1100 4 10 0 7 8 9 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
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1380	GTCAGCCTGAACATAACATCCTTGGGATTACGCTCCCTCAAGGAGATAAGTGATGATGGAGAT	w	da
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1260	ATCACAGGGT	N	DЬ
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1140	AACTGCACCTCCATCAGTGGCGATCTCCACATCCTGCCGGTGGCATTTAGGGGTGACTCC	1081	Db
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                                                                                                                                                                                              GCCACAGGCCAGGTCTGCCATGCCTTGTGCTCCCCCGAGGGCTGCTGGGGGCCCGGAGCCC
                                                                                                                                                                                                                                      TTTGGGACCTCCGGTCAGAAAACCAAAATTATAAGCAACAGAGGTGAAAACAGCTGCAAG
                                                                                                                                                      AGGGACTGCGTCTCTTGCCGGAATGTCAGCCGAGGCAGGGAATGCGTGGACAAGTGCAAG
                                                                                                              CTTCTGGAGGGTGAGCCAAGGGAGTTTGTGGAGAACTCTGAGTGCATACAGTGCCACCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human epidermal growth factor receptor cDNA sequence and aberrant expression of the amplified gene in A431 epidermoid carcinoma cell Nature 309 (5967), 418-425 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 5532)
Ulirich,A., Coussens,L., Hayflick,J.S., Dull,T.J., Gray,A., Tam,A.W., Lee,J., Yarden,Y., Libermann,T.A., Schlessinger,J., Downward,J., Mayes,E.L., Whittle,N., Waterfield,M.D. and
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RSLKEISGGVIISKNILCYANTINKKLFGTSGGKTKIISKRGENSCKATGOVCHA
LCSPEGCWGFEPROCVSCRNUNGWESCYDKCKLLEGEPREFVENSECIOCHPECLPOA
MUITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVMGENNTLVWKYADAGHVCHLCHPNC
TYGCTGPGLEGCPTNGPKIPSIATGMWGALLLLLVVALGIGIFMRRHIYRKFTLRRL
LQERELYEPLTPSGEAPNOALLRILKETEFKKIKVLGSGAPGTVYKGLMIPEGEKVKI
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LDYVREHKONIGSOYLLWCVOIAKCMNYLEDRRLYHRDLAARNYLYKTPOHYKITDE
                                                                                                                                                                         GLAKLLGAEEKEYHAEGGKVPIKWMALESILHRIYTHOSDVWSYGVTVWELMTFGSKP
YDGIPASEISSILEKGERLPQPPICTIDVYMIMVKCWMIDADSRPKFRELIIEFSKMA
RDPQRYLVIQGDERWHLPSPTDSNFYRALMDEEDMDDVVDADEYLIPQQGFFSSPSTS
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NLQIIRGNWYYENSYALAVLSNYDANKTGLKELPMRNLQEILHGAVRFSNNPALCNVE
SIQMRDIVSDFLSNMSMDFQNHLGSCQKCDPSCPAGGEENQQKLTIICAQQ
CSGRCRGKSPSDCCHNQCAAGCTGPRESDCLVCRKFBDEATCKDTCPPLMLYNTTYQ
MDVNPEGKYSFGATCVKKCPRNYVYTDHGSCVRACGADSYEMEEDGVRKKKCEGPCR
KYCKCIGIGEFKJSLSINATNIXHFKNCTSISGDLHILPVAFRGDSFTHTPPLDPQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
187. .258
                         /note="EGF extracellular domain'
568. .576
                                                                                                                                   RTPLLSSLSATSNNSTVACIDRNGLQSCPIKEDSFLQRYSSDPTGALTEDSIDDTFLP
VPEYINQSVPKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGNPEYLNTVQPTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product--"epidermal growth factor receptor"
/protein_id="CAA25240".1"
/db_xref="G1:757924".1"
/db_xref="SWISS-PROT:P00533"
                                                                                         SEFIGA
                                                                                                              VNSTFDSPAHWAQKGSHQISLDNPDYQQDFFPKEAKPNGIFKGSTAENAEYLRVAPQS
/note="Asn-linked glycosylation site"
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187. .3819
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                                                                                                                                 ACCATCCAGGAGGTGGCTGGTTATGTCCTCATTGCCCTCAACACAGTGGAGCGAATTCCT
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                                            TTGGAAAACCTGCAGATCATCAGAGGAAATATGTACTACGAAAATTCCTATGCCTTAGCA
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1472 a 1484 c 1337 g 1239 t
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/note="Asn-linked glycosylation site"
5512. .5517
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1924. .3732
/note="v-erb B homology"
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772. .780
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/note="Asn-linked glycosylation site"
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/note="Asn-linked glycosylation site"
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/note="Asn-linked glycosylation site"
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/note="Asn-linked glycosylation site"
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Merlino,G.T., Ishii,S., Whang-Peng,J., Knutsen,T., Xu,Y.-H., Clark,A.J.L., Stratton,R.H., Wilson,R.K., Ma,D.-P.P., Roe,B., Hunts,J.H., Shimizu,N. and Pastan,I. Structure and localization of genes encoding aberrant and no epidermal growth factor receptor RNAs from A431 human carcin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comparative genomic sequence analysis and isolation of human and mouse alternative egfr transcripts encoding truncated receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2864)
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Direct Submission
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                                                                   /Protein_id="AAG43240.1"
/db_xref="G1:12002212"
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/translation="MRPSGTAGAALLALAALCPASRALEEKKVCQGTSNKLTQLGTE
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EDHFLSLQRWFNNYYSWFALAVLSWYDANKTGLKELPHENLQEILHGARESNHPALCNVE
SIQWRDIVSSDFLSNMSMDFQNHLGSCQKCDPSCPNGSCWAGAGEENCQKLTKIICAQQ
CSGRCRGKSPSDCCHNQCAACCTGPRESDCLVCRKFRDLATCKDTCPFLHLYNPTYYQ
CSGRCRGKSPSDCCHNQCACCTGPRESDCLVCRKFREDEATCKDTCPFLHLYNPTYYQ
MDVNFBGKYSFGATCVKKCPRNYYVTDHGSCVRACGADSYEMEEDGVRKCKKCBGPCR
KVCNGIGIGEFKDSLSINATNIKHFKNCTSISGDLHILPVAFRGDSFTHTPPLDPQEL
DILKTVKEITGFLLIQAWPENRTDLHAFENLEIIRGRTKQHGQFSLAVVSLNITSLGL
RSLKEISDGDVIISGNKNLCYANTINWKKLFGTSGQKTKIISNRGENSCKATGQVCHA
                                                                                                                                                                                                                                                         precursor"
                                                                                                                                                                                                                                                                                                                               /note="ERBH1; alternative transcript encoding only the
extracellular domain of the receptor"
                                                                                                                                                                                                                                                                                   /product="truncated epidermal growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="7p11.2-p12"
/tissue_type="placenta"
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661 gggcgctgccgtggcaagtcccccagtgactgctgccacaaccagtgtgctgcaggctgc
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TYGPGNESLKAMLFCLFKLSSCNQSNDGSVSHQSGSPAAQESCLGWIPSLLPSEFQLG
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Local Similarity

79.08; 99.98;

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1 (bases 1 to 2393)

Xu,Y.H., Ishii,S., Clark,A.J., Sullivan,M., Wilson,R.K., Ma,D.P., Roe,B.A., Merlino,G.T. and Pastan,I.

Human epidermal growth factor receptor CDNA is homologous to a variety of RNAs overproduced in A431 carcinoma cells

Nature 309 (5971), 806-810 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-MAY-1985) to the EMBL/GenBank/DDBJ databases Data kindly reviewed (28-05-1985) by Merlino G.
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AFENLEIIRGTKOHGGFSLAVVSLNITSLGLISLKEISGDVIISGNKHLCYANTIN
WKKLFGTSGOKTKIISNRGENSCKATGGVCHALCSPEGCWGPEPRDCVSCRNVSBGRE
CVDKCHLLEGEPREFVENSEGIGCHPECLPOAMNITGTGRAPDHGIOGAHYIDGPHGV
KTCPPAGVMGENNITLWKYADAGHYCHLCHPNCTVGCGTGFGLEGGFTNGFKIPSIATGM
VGALLLLLLVVALGIGLFMRRRHIVRKFTLRRLLQERELVEPITPSGEAPPNQALLBILK
                                                                                                     ETEFKKIKVLGSGAFGTVYKGLMIPEGEKVKIPVAIKELREATSPKANKEILDEAYVM
ASVDNPHVCRLLGICLTSTVQLITQLMPFGCLLDYVREHKDNIGSQYLLNMCVQIAKG
MNYLEDRRLVHRDLAARNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKMMA
                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SWISS-PROT:P00533"
/translation="ILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMDFQNHLGS
COKCDPSCPNGSCWGAGEENCOKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGPR
                                                                                                                                                                                                                                                                                                                                                    ESDCLVCRKERDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVT
DHGSCVRACGADSYBMEEDGVRKCKKCEGPCRKVCNGTGTGEFKDSLSINATNIKHFK
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/db_xref="GI:4378981"
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                                                                                ESILHRIYTHQSDVWSYGVTVWELMT#GSKPYDGIPASEISSILEKGERLPQPPICT,
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                                                                                                             ACCTCCGGTCAGAAAACCAAAATTATAAGCAACAGAGGTGAAAAACAGCTGCAAGGCCACA
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                                                                ATTTCAGGAAACAAAATTTGTGCTATGCAAATACAATAAACTGGAAAAAACTGTTTGGG
                                                                                                                                                                                                                                       CTGAACATAACATCCTTGGGATTACGCTCCCTCAAGGAGATAAGTGATGGAGATGTGATA
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Paria,B.C., Das,S.K., Andrews,G.K. and Dey,S.K.
Expression of the epidermal growth factor receptor gene is regulated in mouse blastocysts during delayed implantation proc. Natl. Acad. Sci. U.S.A. 90 (1), 55-59 (1993)
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/db_xref="MGD:MGI:95294"
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RLLQERELVEPLTPSGEAPNOAHLRILKETEFKKIKVLGSGAFGTVYKGLMIPSGEKV
KIPVAIKELREATSPANNEZILBEAYVAASUNDHVCRILGICLTSTVOLITQLMPYG
CLLDYVREHKDNIGSOYLLNMCVQIAKGMIYLEDRRLVHRDLAARNVLVKTPQHVKIT
DFGLAKLLGAEEKEYHAEGGKVPIKMMALESILHRIYTHGDLAARNVLVKTPQHVKIT
DFGLAKLLGAEEKEYHAEGGKVPIKMMALESILHRIYTHGSSWSYGVPWWELMTPGS
KYPQGIPASDISSILEKGBELQPPICTIDVFMINVCMAIDAUSRPKFRELILEESK
MARDPQRYLVIQGDERMHLPSPTDSNFYRALMDEEDMEDVVDADEYLIPQQGFFNSPS
TSRFTULSSLSATSNNSTVACINRRGSCRVKEDAFLQRYSSDFTGAVTEDNIDDAFLP
VEBYVNGSVPFRPAGSVQNPVYHNOPLHPAGFDLHTQNPHSNAYGNPEXLNTAQPTC
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/replace="a"
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EILKTVKEITGELLIQAWPDNWTDLHAFENLEIIRGRTKQHGQFSLAVVGLNITSLGL
RSLKEISDGDVIISGNRNLCYANTINKKKLFGTPNOKTKINNNRAEKDCKAVNHVCNP
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MDVNPEGKYSFGATCVKKCPRNYVYTDHGSCVRACGPDYYEVEEDGIRKCKKCDGPCR
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TIQWRDIVQNYFMSNMSHDLQSHPSSCPKCDPSCPNGSCNGGGEENCQKLTKKIICAQQ
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WNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGIMGENNTLVWKYADANNVCHLCHANC
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Comparative genomic sequence analysis and isolation of human and
                                                                                                                                                                     Submitted (07-JUN-2000) Department of Cell Biology, Vanderbilt University, 1161 21st Ave. S. Nashville, TN 37232-2175, USA
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    /gene≃"Egfr"
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                                                                                      /organism="Mus musculus"
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MNITCUGREGDNCIOCAHYLDGEHCVKTCAGIMGENNTLYWKYADANNVCHLCHANC
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TSRTPLLSSISATSNNSTYACINRNGSCRVKEDAFLQRYSSDPTGAVTENNIDARFLF
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TIGWRDIVQNYEMSNNSMDLQSHESSCERCDESCENGSGGERENGKLTKIICAQQ
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481 agcatccagtggcgggacatagtcagcagtgactttctcagcaacatgtcgatggacttc 540 121 ttgggcacttttgaagatcattttctcagcctccagaggatgttcaataactgtgaggtg 180 644 CAGGAAATCCTGATTGGTGCTGTGCGATTCAGCAACAACCCCATCCTCTGCAATATGGAT 584 ATCCTGTCCAACTATGGGACAAACAGAACTGGGCTTAGGGAACTGCCCCATGCGGAACTTA 344 CTGGGCACTTTTGAAGACCACTTTCTGAGCCTGCAGAGGATGTACAACAACTGTGAAGTG 224 ATGCGACCCTCAGGGACCGCGAGAACCACACTGCTGGTGCTGCTGACCGCGCTCTGCGCC 283 ACTATCCAGTGGAGGGACATCGTCCAAAACGTCTTTATGAGCAACATGTCAATGGACTTA TTGGAGAACCTGCAGATCAGGGGAAATGCTCTTTATGAAAACACCTATGCCTTAGCC accatccaggaggtggctggttatgtcctcattgccctcaacacagtggagcgaattcct GCAGGTGGGGCGTTGGAAGAAAAGAAAGTCTGCCAAGGCACAAGTAACAGGCTCACCCAA 343 ttggaaaacctgcagatcatcagaggaaatatgtactacgaaaattcctatgccttagca 360 ACCATCCAGGAGGTGGCCGGCTATGTCCTCATTGCCCTCAACACCGTGGAGAGAATCCCT 0; Mismatches 333; Indels Score 1484.2; Pred. No. 0; DB 10; Length 5935; 6; 300 240 463 403 1.

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Rattus norvegicus
Eukaryota; Metazoa; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (30-NOV-1999) Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Manning Dr, Chapel Hill, NC 27599-7295, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-NOV-1991) Lineberger Comprehensive Cancer Center, University of Worth Carolina at Chapel Hill, Manning Dr. Chapel Hill, NC 27599-7295, USA 3 (bases 1 to 4194)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence update by submitter on Nov 30, 1999 this sequence version replaced gi:204000
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                                 /gene="Egfr"
154. .3783
                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/strain="Fisher"
                                                                                                               /dev_stage="adult"
1. .4194
                                                                                                                                                                                              /tissue_type="liver"
                                                                                                                                                                                                                               /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
/gene="Egfr"
                                                                                                                                                                                                                                                                /db_xref="taxon:10116"
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                          CAGGAAATTCTGATCGGTGCTGTGCGATTTAGCAACAACCCCATCCTCTGCAATATGGAG 633
                                                                                                                                                                                                                                                                                                                                                                          caggaaatcctgcatggcgcgtgcggttcagcaacaaccctgccctgtgcaacgtggag 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gtcttatctaactatgatgcaaataaaaccggactgaaggagctgcccatgagaaattta 420
                                                                                                                                                                                                              agcatccagtggcgggacatagtcagcagtgactttctcagcaacatgtcgatggacttc 540
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/product="epidermal growth factor receptor"
/db_xref="epidermalgrowth.
/d
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1680	ttctggagggtgagccaagggagtttgtggagaactctgagtgcatacagtgccaccc	1621	Qy
1773	ACGGACTGTGTCTCCTGCCAGAATGTGAGCAGAGGCAGGGAGTGCGTGGACAAGTGCAAC		дb
1620	gygactgcytottotogogaatytcagogagycagggaatycytggacaagtycaa	i.s	Qy
1713	GCCACGAACCACGTCTGTAATCCTTTATGCTCCTCGGAAGGCTGCTGGGGCCCTGAGCCC	1654	Db
1560	ocacaggocaggictgccatgccttgtgctcccccgagggctgctgcggggccggagcc	ū	Qy
1653	TTCGGGACGCCCAATCAAAAGACCAAAATCATGAACAACAGAGCTGAAAAAGGACTGCAAG	S	Дb
1500	, tigggacctccggtcagaaaaccaaaattataagcaacagaggtgaaaacagctgcaa	4	Qy
1593	GTGATTATTTCTGGGAACCGGAAATTTGTGCTACGCAAACACTATAAACTGGAAAAAACTC	1534	Db
1440	tgataatttcaggaaacaaaaatttgtgctatgcaaatacaataaactggaaaaaaac	نبا	Qy
1533	GTCGGCCTGAACATAACATCGCTGGGGTTGCGTTCCCTCAAGGAGTCAGTGATGGGGAT	4	Db
	tcagcctgaacataacatccttgggattacgctccctcaaggagataagtgatgga	1321	QΥ
1473	GTTTTCTCTGGCGG	4	dd
1320	agaacctagaaatcatacgcggcaggaccaagcaacatggtcagttttctctttgcagt	N	Qy
1413	ATAACAGGGTTTTTGCTGATTCAGGCTTGGCCTGAAAACTGGACTGACCTCCATGCTTTT	1354	망
N	tcacagggtttttgctgattcaggcttggcctgaaaacaggacggac	N	ΟУ
1353	TCACCCGCACTCCTCTAGACCCACGGGAACTAGAAATTCTCAAAACTGTGAAGGAA	1294	DЬ
2	toacacatactcctcctctggatccacaggaactggatattctgaaaaccgtaaagga	1141	QΥ
1293	TACTGCACTGCCATCAGTGGGGACCTCCACATCCTGCCAGTGGCCTTTAAGGGGGGATTCT	N	B
1140	actycacctccatcagtygcgatctccacatcctgccggtggcatttaggggtgactc	0	Qy
23			Db 45
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1020	acggcgtccgcaagtgtaagaagtgcgaagggccttgccgcaaagtgtgtaacggaat	961	Q _V
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960	tgacagatcacggctcgtgcgtccgagcctgtggggccgacagctatgagatggagga	901	Qy
0	CCTGAGGGGAAGTACAGCTTTGGTGCCACCTGTGTGAAGAAATGCCCCAGAAACTACGTG	994	B 4
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91232866
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X59698.1 GI:50803
EGF receptor; EGFR gene.
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Mammalla: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2301)
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EDHFISLQRWYNNCEVVLANLETTY VQRWYDLSFLKT I QEWAGYVLI ALMYVERI PLE
RUALI IRGNALY ENIY ALA ILSNWGTNETGLREIL PRINNLOE ILIGAWRESNIP FLC NMD
TIQWRD I VQNVFMSNMSMDLQSHPSSCPKCDPSCPNGSCWGGGEERIQGKLTK I I CAQQ
CSHRCRGRSPSDCCHNQCAAGCTGPRESDCLVGKFQDEATCKDTCEPILMLYNPTTYQ
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EILKTYKETTGFLLIQAMPDNMYDLHAFENLEI I RGRTKQHGQFSTRXP PLDPREL
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RSLKEI SDGDVI I SGNRNLCYANT I NWKKLFGTPNQKTKI NNNRAEKDCKAVNHVCNP
LCSSEGCWGPEPRDCVSCQNVSRGRECVEKWILLEGEPREFVENSDCIQCHPECLPQA
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604 c 597 q 4
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/db_xref="GI:50804"
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/db_xref="taxon:10090"
/tlssue_type="brain"
/clone_ib-"lambda gtil cDNA library"
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                                                                                                                                                                                                                                                                                       /db_xref-"MGD:MGI:95294"
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Matches 1698; Query Match Best Local :

Similarity

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Conservative

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Luetteke, M.C., Phillips, H.K., Qiu, T.H., Copeland, N.G., Earp, H.S., Jenkins, N.A. and Lee, D.C.
The mouse waved-2 phenotype results from a point mutation in the ECF receptor tyrosine kinase ECF receptor. 8, 399-413 (1994)
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NLOI IT GRANLY ENTY PALAL LISUNGTNREG LERLBARRIJGE LLI GAVRE SUNPI LCAMD

TIQMRDI VQNYPMSNNSMDLQSHPSSCPKCD PSCP NGSCWGGGEENCQKLTK I I CAQQ

CSHRCRGRSSDCCHNQCAAGCTG PRESDCLVCQK FORGACKDTC PLALLY NFTTYQ

CSHRCRGRSSDCCHNQCAAGCTG PRESDCLVCQK FORGACKDTC PLALLY NFTTYQ

MDVNPEGKY STGARCVKKC PRAY VYDDHGSCYVRACGEDY LEVEEDGA I RKCKKCDGPCR

KVCNG I GIGEFKDTLS I NATNI KHFKYCTA I SGDLH I LPVAFKGDSFTRTPPLDREL

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/tissue_type="liver"
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REFERENCE AUTHORS

SOURCE ORGANISM **TOCUS** KEYWORDS VERSION ACCESSION DEFINITION house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 2618)

Reiter J.L., Threadgill, D.W., Eley, G.D., Strunk, K.E.,

Danielsen, A.J., Schehl Sinclair, C., Pearsall, R.S., Green, P.J.,

Yee, D., Lampland, A.L., Balasubramaniam, S., Crossley, T.D., AF124513 2618 bp mRNA ROD 26-JAN-: Mus musculus epidermal growth factor receptor (Egfr) mRNA, alternatively spliced, complete cds. AF124513 AF124513.1 GI:5524152 26-JAN-2001

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Comparative genomic sequence analysis and isolation of human and mouse alternative egfr transcripts encoding truncated receptor
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NLOI IRGNALYENTYALAILSNCTUNFFGLERLDWRRLDEILIGAVRESNNEILGNMD
TIOWRDIVONVEMSNNSMDLOSHPSSCPKCDPSCPNGSCMGGEENCQKLTXIICAOO
CSHRCRGRSPSOCCHNOCAAGCTGPRESDCLVCOKFODEATCKNTGCPLALLYNPTTYO
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MNITCTGRGPDNCIQCANYIDGPROVSTCPAGJMGENNTLVWKYADANNYCHLCHANC
TYGCAFFELJOGCENPSGGYPGWOAILKTFWI"

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="11"
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/protein_id="AAD44149.1"
/db_xref="G1:5524153"
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/note="Erbbl; alternatively spliced"
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Direct Submission
Submitted (07-FEB-1996) Jill L. Reiter,
Submitted (07-FEB-1996) Jill L. Reiter,
Blology, Mayo Clinic, 200 First St. SW,
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Reiter, J.L. and Maihle, N.J.

A 1.8 kb alternative transcript from the human epidermal growth factor receptor gene encodes a truncated form of the receptor Nucleic Acids Res. 24 (20), 4050-4056 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1593)
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NLQIIRGNMYYENSYALAVLSNYDANKTGLKELPMRNLQEILHGAVRFSNNPALCNVE
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/db_xref="GI:1628550"
/translation="MRPSGTAGAALLAILAALCPASRALEEKKVCQGTSNKLTQIGTF
                                                                                                                    /gene="EGFR"
245. .1462
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/tissue_type="placenta"
1. .1456
                                                                                                                                                             /gene="EGFR"
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/db_xref="taxon:9606"
/chromosome="7"
                                                                                                     /note="ErbB1-S"
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CSGRCRGKSPSDCCHNQCAAGCTGPRESDCLVCRKFRDEATCKDTCPPLMLYNPTTYQ
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                                                        GTGACAGATCACGGCTCGTGCGTCCGAGCCTGTGGGGCCGACAGCTATGAGATGGAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-MAR-1997) Obstetrics & Gynecology, University Illinois at Chicago, 820 S. Wood Street, Chicago, IL 60612, please also see Ilekis, J. in RK Miller, HA Thiede (eds): 'Molecular Biology and Cell Regulation of the Placenta.' New Plenum, 103-117, 1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        llekis,J.v., Gariti,J., Niederberger C.
Expression of a Truncated Epidermal Gro
Protein (TEGER) in Ovarian Cancer
Gyn. Onc. 65 (1997) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ilekis, J. V., Stark, B.C. and Scoccia, B. Possible role of variant RNA transcripts in epidermal growth factor receptor expression Mol. Reprod. Dev. 41 (2), 149-156 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1868)
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/db_xref="taxon:9606"
/tissue_type="placenta"
504. .575
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                      /translation="mrpsgtagaallallaalcpasraleekkvcogtskkltqlgteebherscheekkvcogtskkltqlgteebherscheekkvcogtskkltqlgteebherscheekkvcogtskkltqlgteebherscheekkvlgeleekkvcogtskkltqlktyvertplekkvltgellekkvertplekkvltgelekkvltglekekkvltglekekkvltglekekkvltglekekkvltglekekkvltglekekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltglekkvltgle
                                                                                                                                                                                     /product-"truncated epidermal growth protein precursor" /protein_d="An#53063.1" /db_xref="GI:2051985"
                                                                                                                                                                                                                                                                                                /note="TEGFR; the calculated molecular weight of the nascent protein is approximately 42 kD (includes signal peptide at amino acid positions 1-24); the molecular weight of the mature protein is approximately 80 kD; secreted growth factor receptor"
    DILKTVKEITGLS"
                                                                                                                                                                                                                                                                               codon_start-
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540 983 480 923 420 863 360 300

803

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623 120 563 60

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960

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780

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Search completed: January 14, 2002, 20:13:47 Job time: 4172 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  2034
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1207.8
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2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn/NA1987.DAT:*
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11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
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                                        AAF85332
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                                                                                                       cDNA sequence enco
Human EGF receptor
pRLD1D2D3.ApaL con
pRLD2D3D4 construc
Epidermal growth f
                                                                                                                                                                                                                                                            Description
                                    EGF receptor relat pRLD3D4 construct. Human inducible ni
  HER4. Homo sapien
Receptor tyrosine
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Probe #1662 used	AA101671	22	486	6.7	137	5
Probe #1736 used	AAI33050	22	486	6.7	137	44
Probe #1676 for	AAI11743	22	486		1'37	ū
#6658	AAI06667	22	220		137	2
Probe #14885	AAI46199	22	220		137	41
Probe #10888	AAI20955	22	220		137	0
DNA fragment of	AAC61546	21	1033		149	9
DNA fragment of	AAC61547	21	172		172	8
	AAQ06828	11	1872	9	391	7
EGRF-R erbB-3	AAQ12224	12	4545		392	5
Nucleotide sequenc	AAH42210	22	3771		10	ű
Mouse Her-2/neu cD	AAA89737	21	3771		in	4
DC8scFv-erbB2EC	AAZ50586	21	2871		400.6	ũ
Her2-GM-CSF immuno	AAT72725	18	2385		\circ	ö
Rat HER-2/neu prot	AAA89753	21	3955		$\overline{}$	Ξ
Rat neu promoter.	AAT01590	16	3955		0	ā
HER-3 epithelial	AAQ13363	12	4978		\circ	ě
E3-16 cDNA clone	AAX60313	20	4905	20.1	409.4	28
ω	AAV58734	19	4905		409.4	7
	AAT10059	17	4905		409.4	9
HER-2 nucleic acid	AAZ31071	20	4473		417.4	ű
cDNA encoding the	AAA14812	21	4472		17	4
Sequence encoding	AAQ46083	14	4299		417.4	ũ
Human HER-2/neu	AAH23392	22	3768	٠	17,	ŭ
Human HER-2/neu on	AAX01912	20	3768			ŭ
HER-2/neu oncogene	AAT40739	17	3768		~	õ
Human HER-2/neu co	AAA89736	21	3600		417.4	ڡؘ
HER2 transgene pla	AAF24297	22	9274		419	œ
Nucleotide sequenc	AAZ60815	21	4530		419	7
Human HER2 gene	AAT71253	18	4530		419	Ġ
Her-2/neu (ERBB2/c	AAT01585	16	4530		419	'n
Human heregulin	AAA09455	21	3768		419	4
Receptor tyrosine	AAT18533	17	5555		431	w
TOTAL STORY OF COLUMN						

ALIGNMENTS

RESULT AAF85332 19-NOV-1999; 99US-0166594 19-NOV-1999; 99US-0444038 30-MAR-2000; 2000US-0539248 Epidermal growth factor receptor 1; EGFR1; cell surface marker; protein-tyrosine kinase receptor; PTKR; immunoselection; gene therapy; bone marrow transplant; graft facilitation; immune reconstitution; ss. AAF85332; AAF85332 standard; DNA; 3633 BP (NOVS) NOVARTIS AG. Homo Nucleotide sequence of wild type EGFR1. 23-JUL-2001 (first entry) 17-NOV-2000; 2000WO-EP11474 25-MAY-2001. WO200136659-A2 H sapiens /*tag= a /transl_except= "(pos: 1618..1620, aa: Asn)" /product= "EGFR1" Location/Qualifiers . . 3633

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Matches 2034; Conserv
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The specification describes a method for diagnosing glioma in a brain cell sample suspected of being cancerous. The method comprises detect the presence of a nucleic acid encoding an epidermal growth factor
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01-NOV-1991;
05-MAR-1986;
                                     This invention describes a novel purified nucleic acid (I) (v-erbB related gene) specifically hybridizing to all or part of a MACI17 gene and not hybridizing to nucleic acid encoding an epidermal growth factor receptor. The product of the invention has anticancer and cytostatic activity. Antibodies to the protein encoded by (I) are conjugated to toxins and kill cancer cells expressing (I). Antibodies to the protein encoded by (I) are useful for the treatment of cancer. Fragments of (I) and the MACI17 gene are useful as probes for the detection of human mammary carcinoma or other malignancies resulting from the v-erbB related gene. This sequence encodes a human epidermal growth factor (EGF)
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Sequence 5532 BP; 1472 A; 1484 C; 1337 G; 1239 T;
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RESULT AAQ43812 AAQ43812 standard; DNA; 6274 BP 4

20-OCT-1993 (first entry)

pRLD1D2D3.ApaL construct.

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Epidermal growth factor receptor truncate protein; EGF; growth; binding sites; adsorptive agents; mammallan cell growth abnormality; detection; reproduction; signal transmission; pRLDID2D3ApaL; ds.

Synthetic.

Key

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                 ery Match
Best Local Similarity
Matches 1587; Conser
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The sequence is that of the pRLD2D3D4 construct which encodes the epidermal growth factor (EGF) receptor truncate protein in 102D3D4 having EGF binding sites. The protein binds ligands of the EGF receptor without transmitting a signal for the growth and reproduction of a cell. It can be used as an adsorptive agent for any moleties that bind the EGF receptor as the portal of entry to a cell. It competes with the EGF receptor present on the cell surface for the binding of ligands and thereby inhibits the action of the ligands or prevents the entry of viruses into cells. It can also be used as for the EGF receptor itself, such as in the detection of abnormalities in mammalian cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epidermal growth factor receptor truncate protein; EGF; binding sites; adsorptive agents; mammalian cell growth abnormality; detection; growth; reproduction; signal transmission; ds.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This DNA encodes an epidermal growth factor (EGF) receptor related protein (ERRP). The ERRP is highly homologous to the mouse EGFR and a truncated rat EGFR. The ERRP can be expressed by standard recombinant methodology. The ERRP acts as a EGFR receptor modulator. The ERRP acts when transfected into colon cancer cell line is useful for inhibiting proliferation of the cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel epidermal growth factor receptor related protein and polynucleotide useful for inhibiting proliferation of cancer cell line
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P-PSDB; AAB48033.
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                  661 gggcgctgccgtggcaagtcccccagtgactgctgccacaaccagtgtgctgctgcaggctgc 720
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Pred. No. 3.1e-274;
0; Mismatches 220;
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12-JUN-1990;
                           12-JUN-1990;
                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                            pRLD3D4 construct.
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900S-0536B96
                         90us-0536896.
                                                                                                                                    Location/Qualifiers 1077..1079
                                                                                                         /note- "codon ARA encodes Ile"
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Matches 984; Query Match Best Local Similarity

Conservative

0; Mismatches

5; Indels

0

Score 981; DB 14; Length 5750; Pred. No. 8.2e-271;

48.2%;

Sequence 5750 BP; 1367 A; 1479 C; 1536 G; 1367 T; 1 other;

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The sequence is that of the pRLD3D4 construct which encodes the epidermal growth factor (EGF) receptor truncate protein LD3D4 having EGF binding sites. The protein binds ligands of the EGF receptor without transmitting a signal for the growth and reproduction of a cell. It can be used as an adsorptive agent for any moletles that bind the EGF receptor as the portal of entry to a cell. It competes with the EGF receptor present on the cell surface for the binding of ligands and thereby inhibits the action of the ligands or prevents the entry of viruses into cells. It can also be used as for the EGF receptor itself, such as in the detection of abnormalities in mammalian cell growth. It is also useful for preps, novel receptors for efficient detection of ligands and their anti-agonists or agonists. The features table indicate a discrepancy between the LD3D4 protein sequence given in the specification and that which the pRLD3D4 DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New epidermal growth factor receptor truncate proteins \cdot which bind ligands of EGF receptor without transmitting signal for growth
                                         given in the specification would encode
                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 9; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WARN ) WARNER LAMBERT CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to antisense compounds, especially oligonucleotides, which are targeted to a nucleic acid encoding inducible nitric oxide synthase and which specifically hybridise to and modulate expression of inducible nitric oxide synthase. The antisense compounds have immunomodulator, antidiabetic, cardiovascular, cardiant, have immunomodulator, antidiabetic cardiovascular, cardiant, neuroprotective, disorder and vasotropic activity. The antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for treating e.g. immunological, cardiovascular or neurological disorders, or ischaemia \,
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                                                                                                                                                               Matches 991;
                                                                                                                                                                                                                                                                   HER4 is the fourth member of the EGFR-family of tyrosine kinases and is expressed in some human cancers and in some tissues of neuronal or muscle origin. HER4 polynucleotides, opt. labelled, are useful in assays (e.g. of HER4 mRNA to detect certain neoplasms, esp.
                                                                                                                                                                                                                                                                                                                                                                            New recombinant nucleic acid expressing HER4 - a new receptor tyrosine kinase expressed in some cancer cells, and related vectors, antibodies, ligands etc. for diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human epidermal growth factor receptor; HER; EGF; tyrosine kinase; cancer; neuronal tissue; muscle tissue; neoplasm; carcinoma; primer; probe; PCR; ss.
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                                                                                                                                                                                                                              Sequence 5501 BP; 1605 A; 1173 C; 1230 G; 1493 T; 0 other;
                                                                                                                                                                                                                                                         breast carcinoma) and as primers in PCR or as probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-169599/21.
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1220 ttcaggcttggcctgaaaacaggaccggacctccatgcctttgagaacctagaaatcatac 1279
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1340 ccttgggattacgctccctcaaggagataagtgatggagatgtgataatttcaggaaaca 1399
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                                     14-OCT-1994;
                                                                                                                                                                 mat_peptide
                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                              HER4/pl80erbB4; HER4; receptor tyrosine kinase;
epidermal growth factor receptor; cancer; diagnosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                   05-JUL-1996 (first entry)
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         (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                  10-OCT-1995;
                                                                                              25-APR-1996
                                                                                                                         W09612019-A2
                                                                                                                                                                                                                                                                                                                                           Receptor tyrosine kinase HER4 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5501 BP; 1606 A; 1173 C; 1229 G; 1493 T; 0 other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Culouscou J, Hellstrom I,
Shoyab M, Slegall C;
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                                                                                                                                                                                     is expressed in some human cancers and in some tissues of neuronal or muscle origin. HER4 polynucleotides, opt. labelled, are useful in assays (e.g. of HER4 mRNA to detect certain neoplasms, esp.
                                                                                                                                                                                                                                 This sequence is identical with that of HER4 (AAQ64896) up to nucleotide 3168, where the sequence diverges and the ORF stops after 13 amino acids, followed by an extended, unique 3'-UTR. HER4 is the fourth member of the EGFR-family of tyrosine kinases and
                                                                                                                                                                                                                                                                                                                                                            New recombinant nucleic acid expressing HER4 - a new receptor tyrosine kinase expressed in some cancer cells, and related vectors, antibodies, ligands etc, for diagnosis and treatment of
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                                                                                                                                        Sequence 5555 BP; 1746 A; 1054 C; 1106 G; 1647 T; 2 other;
                                                                                                                                                                                                                                                                                                               Claim 1; Fig 2A; 104pp; English
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83 agaaagtttgccaaggcacgagtaacaagctcacgcagttgggcacttttgaagatcatt 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A DNA sequence (AAT18533) isolated from a human breast MDA-MB-453 library is identical to DNA (AAT18532) coding for novel prototype receptor tyrosine kinase HER4 up to nucleotide 3168, but then abruptly diverges into an apparently unrelated sequence. It codes for an HER4 (AAR91734) that lacks the C-terminal autophosphorylation domain of prototype HER4 (AAR91733). A second alternative HER4 (AAR18534) sequence was also isolated. HER4 polynucleotides can be used in the prepn. of HER4 expression vectors, primers and probes to detect and/or clone HER4, and diagnostic reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding receptor tyrosine kinase, HER4 - related to human epidermal growth factor receptor, used for diagnosis and therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Culouscou J,
Shoyab M, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_difference 4770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5555 BP; 1748 A; 1053 C; 1105 G; 1647 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 124-125; 203pp; English
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P-PSDB; AAR91734.
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                 440 ccgtgcggttcagcaaccatgccctgtgcaacgtggagagcatccagtggcgggaca 499
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Siegall C;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 5.9e-113;
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                                                                        1484 gaatagtaatccgggacaacagaaaagctgaaaattgtactgctgaaggaatggtgtgca 1543
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              fibroblast growth factor 8b (PGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 Breel group derived from the Cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and
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                                                                                                          The claims detail a method for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (i.e. self-proteins), for example, human prostate specific membrane antigen (PSM), hereguin 2 (Her2) and/or fibroblast growth factor 8b (PGF8b). The method comprises effecting
human/murine FGF8b comprising a substantial part of all known and
                                                                                                                                                                                                                       Claim 62; Page 187-193; 220pp; English.
                                                                                                                                                                                                                                                          Inducing immune responses to weakly immunogenic, peptide antigens for the treatment of breast and
                                                                                                                                                                                                                                                                                                                                                                       Gautam A,
                                                                                                                                                                                                                                                                                                                                                                                                                              (MEBI-) M & E BIOTECH AS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;
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                                           896 atgtggtgacagatcacggctcgtgcgtccgagcctgtggggccgacagctatgagatg- 954
                                                                                                                                                                        836 tgaaccccgagggcaaatacagctttggtgccacctgcgtgaagaagtgtccccgtaatt 895
908 acctttctacggacgtgggatcctgcaccctcgtctgccccctgcacaaccaagaggtga 967
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                                                                                                                                                                                                                                                                                                                              668
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                                                                                                                                                                                                                                                                                                                                                                                                   536 acttccagaaccacctgggcagctgcccaaagtgtgatccaagctgtcccaatgggagct 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 gcctcacagagatcttgaaaggagggtcttgatccagcggaacccccagctctgctacc 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386 a-----aaccggactgaaggagctgcccatgagaa 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 gcacccagctctttgaggacaactatgccctggccgtgctagacaatggagacccgctga 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 gaaatatgtactacgaaaattcctatgccttagcagtcttatctaactatgatgcaaata 385
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Oy 1964 Db 1988 Oy 2024	Оу 1910 Дъ 1928	Qy 11 Db 16	ОУ 179 Db 180	Qy 1733 Db 1748	Oy 167 Db 168	Oy 161 Db 162	Qy 155 Db 156	Oy 1493 Db 1508	Qy 1433 Db 1448	Qy 1373 Db 1388	Оу 1313 Db 1328	Qy 1253 Db 1268	Qy 1193 Db 1208	Oy 113	Оу 1 Db 1	оу 1 1	Db
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2023 2047	1963 1987	1909 1927	1849 1867	1792 1807	1732 1747	1672 1687	1612 1627	1552 1567	1492 1507	1432 1447	1372 1387	1312 1327	1252 1267	1192 1207	1132 1147	1072 1087	1027

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RESULT :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Erb-B2 gene is one of the primary genes responsible for the transition of normal breast epithelial cells towards carcinoma in situ and the subsequent development of invasive and metastatic cancer. HPBF (see AAR77093-94), the Erb-B2 promoter binding protections of the property of the primary genes responsible for the prim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New purified protein binding to the ERBB2 gene promoter - to cell proliferation, diagnostic of breast cancer, also related antibodies, nucleic acid, assays and methods for screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4530 BP; 922 A; 1382 C; 1346 G; 880 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed from retro virus or other gene therapy vectors.
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Similarity 52.8%;
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ALIGNMENTS

REFERENCE AUTHORS	TITLE JOURNAL MEDLINE BURMED	REFERENCE AUTHORS	TITLE JOURNAL MEDLINE	ORGANISM	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 AK004911 LOCUS DEFINITION
3 (bases 1 to 2456) 3 (bases 1 to 2456) 3 (bases 1 to 2456) Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikogami,T., Kashiwagi,K., Yujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,	Normalization and subtraction of cap-trapper selected cuass to prepare full-length cDNA libraries for rapid discovery of new genes Genome research. 10 (10), 1617-1630 (2000) 20499374	10349636 2 (bases 1 to 2456) 2 (bases 1 to 2456) Carpinoi, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Carninci, P., and Hayashizaki, Y. High-efficiency full-length cDNA cloning Methods in enzymology. 303, 19-44 (1999) 99279253	<pre>clone_lib:RIKEN full-length enriched mouse cDNA library clone:1300005M11. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1</pre>	AK004911 GI:12836452 CAP trapper. Mus musculus (strain:C578L/6J) adult male liver cDNA to mRNA,	AKO04911 2456 bp mRNA HTC 05-JUL-2001 Mus musculus adult male liver cDNA, RIKEN full-length enriched

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E 5 (bases 1 to 2456)

S Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Kawai, J., Mara, A., Hayatsu, N., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kaco, H., Kawai, J., Mara, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Kojima, Y., Konno, H., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinayawa, A., Shiraki, T., Sogabo, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Yoshida, K., Yoshida, K.
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Submitted (10-1000) Yoshihide Hayashizaki, The Institute of Submitted (10-111-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama 11stitute; 1-7-25 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
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NLOJIFGNALYENYTALAILSNYGTNERGLRELPMRHÖEILIGAMFESNNPILCNM
TIQMRDIVONVFMSNMSMDLØSHPSSCFKCDPSCPARSCMEGGERNCQKLTKIICAQQ
CSHRCKGRSPSDCCINQCAAGCTGPESDCLVCQKFQDEATCKDTCPLLLXNPTYQ
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EILKTVKEITGFLLIQAMPDNWTDLHAFENLEIIRGRTKQHGQPSLAVVGLNITSLGL
RSLKEISDGVIISONRILCYANTINWKLEGSPREFYENSECIGCHPECLPQA
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256. 2223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organismo"Mus musculus"
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[5] GAGACAGGACCGCCCCAACTCGATTTTTTTTTTTTTTTT	URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216) COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse fissues. First strand CDNA was primed with a primer	Okido,T., Owa.C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinaqawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y. TITLE Direct Submission Direct Submission Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Physical and Chemical Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaqawa 230-0045, Japan (E-mail:genome-rse@sc.riken.go.jp,	TITLE Functional annotation of a full-length mouse cDNA collection JOURNAL Nature 409, 685-690 (2001) REFERENCE 5 (bases 1 to 2662) AUTHORS Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayateu, N., Hiramoto, K., Hiracka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Koja, S., Kurihara, C., Matsuyama, T., Mivazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Mivazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,	Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. TITLE RIED integrated sequence analysis (RISA) system: 394-format sequencing pipeline with 398 multicapillary sequencer Genome research. 10 (11), 1757-1771 (2000) MEDLINE 20530913 PUBMED 11076861 REFERENCE 4 (bases 1 to 2662) AUTHORS The RIEM Genome Exploration Research Group Phase II Team and the FANYOM Consortium.	TITLE Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes JOURNAL Genome research. 10 (10), 1617-1630 (2000) MEDLINE 20499374 PUBMED 11042159 REFERENCE 3 (bases 1 to 2662) ROTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., AUTHORS Shibata, K., Itoh, M., Aixawa, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, V., Nakamura, S., Sasaki, N., Carninci, P., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,	SOURCE Mus musculus (strain:C57BL/6J) adult male liver cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:1300003K07. ORGANISM Mus musculus Euteria: Chordata: Craniata; Vertebrata: Euteleostomi; Mammalia: Entheria: Rodentia: Sciurognathi; Muridae: Murinae; Mus. REFERENCE 1 (bases 1 to 2662) AUTHORS Carninci,P. and Hayashizaki,Y. TITLE JOURNAL Methods in enzymology. 303, 19-44 (1999) Methods in enzymology. 303, 19-44 (1999) PUBMED 10349636 REFERENCE 2 (bases 1 to 2662) REFERENCE Carninci,P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y. Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

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BASE COUNT
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Shibata, K., Itch, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itch, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Ishikawa, T., Ozawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Mitsunitegrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                       FANTOM Consortium.

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Nature 409, 685-690 (2001)

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Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M.,
                                                                                                                                                                                                                                                                                          The
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Carninci, P. and Hayashizaki, Y.
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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                      Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojina, Y., Konno, H., Kouda, M., Koya, S., Kurlibara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,
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Mammalia; Eutheria; Rodentia;
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submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama (B-mail:genome-res/gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
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TIOWRDIVQNYEMSRWSMLQSHFSSCPXCDDSCPNGSCWGGGERNCOKLTKIICAQQ
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MNITCTGRGPDKGIGCAVHIOGPGCVKTCTAGIMGENNTLVMXYADANNYCHLCHANG
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/db_xref="MGD:MGI:95294"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812,
                                                                       Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama, Mishikawa,T., Nakamura,Y., Sugano,S., Masuho,Y., and Isogai,T. HRI human CDNA project (Ota,T., Suzuki,Y., Saito,K., Ishii,S. Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S. Masuho,Y., Isogai,T.)
                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fax: 81-438-52-3952
Email: genomicsehri.co.jp
HRI human cDNA project; 5'. & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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                                                                                                                                                                                                                                                                                             1200
1260 tgagaacctagaaatcatacgcggcaggaccaagcaacatggtcagttttctctttgcagt 1319
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nes 746; Conserv
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                                                                                     CGTCAGCCTGAACATAACATCCTTGGGATTACGCTCCCTCAAGGAGATAAGTGATGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute: cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3952
Fax: 81-438-52-3952
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Masuho, Y., Isogai, T.)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S., Masuho,Y., and Isogai,T. HRI human CDNA project (Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S.,
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Mammalia; Eutheria;
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/db_xref="taxon:9666"
/clone="plaCE20"
/clone_lib="plaCE2"
/tissue_type="placenta"
/note="vector: pME18SFL3"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                           found through the I.M.A.G.E. Conso. Plate: LLCM523 row: g column: 09 High quality sequence start: 18 High quality sequence stop: 761.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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            235
    Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
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                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; I chases I to 960; NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections of the 
Contact: Robert Strausberg, Ph.D
                                     Unpublished (1999
                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BE272152
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601141248F1 NIH_MGC_9
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Pred. No. 2.2e-164;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1536 cgagggctgctggggcccggagcccagggacttgcttttctttgccggaatttcagccgagg 1595
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                            1896 tottgaaggotgtocaacgaatgggootaagatocogtocatogocactgggatggtggg 1955
                                                                                                                                                        1836 cgccggccatgtgtgccacctgtgccatccaaactgcacctacggatgcactgggccagg 1895
                                                                                                                                                                                                                                                        466 CAAGACCTGCCCGGCAGGAGTCATGGGAGAAAACAACCCCTGGTCTGGAAGTACGCAGA 525
                                                                                                                                                                                                                                                                                                                                                                                    406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 CGAGGGCTGCTGGGGCCCGGAGCCCCAGGGACTCCTCTTGCCGGAATGTCAGCCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 CAACAGAGGTGAAAACAGCTGCAAGGCCACAGGCCAGGTCTGCCATGCCTTGTGCTCCCC 225
586 TCTTGAAGGCTGTCCAACGAATGGGCCTAAGATCCCGTCCATCGCCACTGGGATGGTGGG 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 CCCTCAGGAGATAAGTGATGGAGATGTGATAATTTCAGGAAACAAAAATTTGTGCTATGC 105
                                                                                                                                                                                                                                                                                        AGGACGGGGACCAGACAACTGTATCCAGTGTGCCCACTACATTGACGGCCCCCACTGCGT 465
                                                                                                                                                                                                                                                                                                                                                                                                                    aggacggggaccagactgtatccagtgtgcccactacattgacggcccccactgcgt 1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCTGAGTGCATACAGTGCCACCCAGAGTGCCTGCCTCAGGCCATGAACATCACCTGCAC 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cagggaatgcgtggacaagtgcaagcttctggagggtgagccaagggagtttgtggagaa 1655
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                                                                                                                        CGCCGGCCATGTGTGCCACCTGTGCCCATCCCAAACTGCACCTACGGATGCACTGGGCCAGG
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High quality sequence stop: 751
Location/Qualifiers
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Tissue Procurement: DCTD/DTP
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/lab.host="DH10B (phage-resistant)"
/lab.host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: Core: porgan: ovary; Vector: porgan; Directionally closed into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 256 c 306 g 189 t
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/db_xref="taxon:9606"
/clone="IMAGE:3141346"
/clone_lib="NIH_MGC_9"
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99.1%;
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Pred. No. 1.2e~158;
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                     1460 aaaccaaaattataagcaacagaggtgaaaacagctgcaaggccacaggccacaggtctgcc 1519
                                                                                                                                                                                                          1341 cttgggattacgctccctcaagg-agataagtgatggatggatgtgataatttcaggaaaca 1399
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                                                                                                                   1400 aaaatttgtgctatgcaaatacaataaactggaaaaaactgtttgggacctccggtcaga 1459
157 AAACCAAAATTATAAGCAACAGAGGTGAAAACAGCTGCAAGGCCACAGGCCAGGTCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   706 ACATCG-TCGGAAGCGCACG 724
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                                                                                            97
                                                                                                                                                                                        37 CTTGGGATTACGCTCCCTCAAGGNAGATAAGTGATGGAGATGTGATAATTTCAGGAAACA 96
                                                                                                                                                                                                                                                                                                         Local
                                                                                            AAAATTTGTGCTATGCAAATACAATAAACTGGAAAAAACTGTTTGGGACCTCCGGTCAGA 156
                                                                                                                                                                                                                                                                                    681;
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM812 row: i column: 18
High quality sequence start: 64
High quality sequence stop: 775.
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Tissue Procurement: DCTD/DTP
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                /note-*Organ: ovary; vector: pOTB9; Site_1: XhoI; Site_2: ECCORI; cDNA made by oligo-dT priming. Directionally cloned into ECCRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 264 c 320 g 202 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH108 (phage_resistant)"
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/db_xref="taxon:9606"
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Pred. No. 5.8
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TITLE
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1 (bases 1 to 736)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbb-remail.nih.gov
Tissue Procurement: DCTD/DTP
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601141568F1 NIH_MGC_9 Homo
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BE315382
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (Lini)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                quality sequence stop: 627
Location/Qualifiers
/tissue_types*Badenocarcinoma cell line*
/lab_host**DH10B (phage-resistant)*
/note="Organ: ovary: Vector: poTBF; Site_1: XhoI;
ECORI; cDNA made by oligo-dT priming. Directional
                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3141184"
/clone_iib="NIH_MGC_9"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 798)
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This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (Info@imge.llnl.gov) for further information.
Insert Length: 1042 Std Error: 0.00
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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2 215 c 221 g 167 t
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/lab_host="DH10B"
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/clone="IMAGE:2370045"
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20 밁

Matches 624;

Local

Similarity

Conservative

0; Mismatches

Indels

3; Gaps

1422 aataaactggaaaaactgtttgggacctccggtcagaaaaccaaaattataagcaacag 1481

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 634)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCM812 row: e column: 17
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                                                                                                                                 160 a
                                                                                                                     /tissue_type="adenocarcinoma cell line"
/lab_host="bH10B (phage-resistant)"
/note="0rgan: ovary; Vector: poTB7: Site_1: XhoI; Site_2:
ECRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRJ/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 169 c 188 g 117 t
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3948664"
/clone_lib="NIH_MGC_9"
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1. .634
29.8%;
98.4%;
Score 606.8; DB 10;
Pred. No. 1.6e-147;
                        Length 634;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI740805 BD MRNA EST 19-DEC-1999 wg24008.x1 Soares_NSF_F8_9N_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2366031 3' similar to gb:K03193 EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                  Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-remail.nih.gov
This clone is available royalty-free through LLNL: contact the
IMAGE Consortium (info@image.linl.gov) for further information.
INSEC Consortium (info@image.linl.gov) for further information.
Insert Length: 1250 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 805) NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
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                                                                                                                                                                                                                  primer
                                                                                                                                                                  quality sequence stop: 488.
Location/Qualifiers
                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2366031"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
     /note-*Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                                                                                                                                                                                                                  -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                     634 ACCATNOAGTGGCGGGACATAGTCAGCAGTGACTTTCCTCAGCACATGTCGATGGACTTN 693
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                                                                                                                                                                                                                                                                694 CAGAACCACCTGNGCAGCTGNCAAAAGTG-GATCCCAGCTGTCCCAATGGGAGCTTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGANATCCTGCATGGCGCCGTG-GGTTCAGCAACAACCCTGCCCTTGTGCACGTGGAG
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A1935313 757 bp mRNA EST 08-MAR-2000 wp16907.x1 NCI_CGAP_LI19 Homo sapiens cDNA_clone IMAGE.2465052 3' similar to gb:K03193 EPIDERWAL GROWTH FACTOR RECEPTOR PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Equal amounts of plasmid DNA from five normalized
libraries were mixed, and as circles were made in vitro.
Following MAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified CDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneries: Soares NBHSF pool 1:
105032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NBHSF pool 1:
1758280-760513, 772104-774407 Soares NBHSP pool 1:
1758280-760513, 20136-322823, 326280-32663 Soares MBHOT
pool 1: 73720-726407, 739080-740999 Subtraction by Bento
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Soares and M. Fatima Bonaldo."
a 227 c 222 g 160 t
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                                241 accatccaggaggtggctggttatgtcctcattgccctcaacacagtggagcgaattcct 300
                                                                                                                                                                                                                                                                                                                                                                                           121 ttgggcacttttgaagatcattttctcagcctccagaggatgttcaataactgtgaggtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 GCGAGTCGGGCTCTGGAGGAAAAGAAAGTTTGCCAAGGCACGAGTAACAAGCTCACGCAG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 ATGCGACCCTCCGGGACGGCGGGGCAGCGCTCCTGGCGCTGCTGCGCTCTGCCCG 205
                                                                                                                                                               326 GTCCTTGGGAATTTGGAAATTACCTATGTGCAGAGGAATTATGATCTTTCCTTCTTAAAG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 gcgagtcgggctctggaggaaaagaaagtttgccaaggcacgagtaacaagctcacgcag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gtccttgggaatttggaaattacctatgtgcagaggaattatgatctttccttcttaaag 240
                                                                                                                                                                                                                                                                                                                                   TTGGGCACTTTTGAAGATCATTTTCTCAGCCTCCAGAGGATGTTCAATAACTGTGAGGTG
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.llni.gov/bbrp/image/image.html
Insert Length: 1220 Std Error: 0.00
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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AI935313
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host-"DH108 (phage-resistant)"
/note-"Organ: lung; Vector: pf793D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eco RI adaptors (Pharmacia), cloned into the Not I and E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metastatic)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2465052"
/clone_lib="NCI_CGAP_Lu19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
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he Not I and Eco RI sites of the modified
Library went through one round of
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM190 row: a column: 11
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 635)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_ILb="NRI_MCE_19"
/clone_ILb="NRI_MCE_19"
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/lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
/note-"Organ: brain; Vector: pOTB7; Site_1: XhOI; Site_2:
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/note-"OTBA made by Oligo-dT priming. Directionally
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                                                                                     Email: ogapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Library Arrayed by: Incyte Genomics, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                 found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov
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                                                       GAAGGGAAGTACAGCTTTGGTGCCACCTGTGTGAAGAAGTGCCCCCGAAACTACGTGGTG
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Site_2: Sali; Cloned unidirectionally, Primer: Oli
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
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Search completed: January 14, 2002, 19:35:59 Job time: 1954 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

ce	epidermal growth factor receptor gene JOURNAL Proc. Natl. Acad. Sci. U.S.A. 82 (15), 4920-4924 (1985) MEDLINE 85270438		REFERENCE 1 (bases 1 to 560) AUTHORS Tshii.S., Xu.Y.H., Stratton, R.H., Roe, B.A., Merlino, G.T. and	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	ORGANISM Homo sapiens	SOURCE Homo sapiens DNA.	S		DEFINITION Human epidermal growth factor receptor (EGFR) gene, exon 1.	LOCUS HUMEGERG 560 bp DNA PRI 0/-N		RESULT 1	
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               Submitted (07-FEB-1996) Jill L.
                                                                                                                                                                                                                                                        Human epidermal growth
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839. .>1189
839. .>1347
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979. .>1347
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1593)
Reiter, J. L. and Maihle, N. J.
A 1.8 kb alternative transcript from the human epidermal growth factor receptor gene encodes a truncated form of the receptor Nucleic Acids Res. 24 (20), 4050-4056 (1996)
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1248. .1251
/note="pot. Spl binding site"
1286. .1291
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/note="pot. Spl binding site"

508 c 398 g 231 t
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1102. >1189
/note="A431 EGF receptor (AA 1 - 29) (1189 is 1st base in codon)"
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999. .>1347
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992. .>1347
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899. .>1347
/note="altern. primary transcript"
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/db_xref="GI:31119"
/db_xref="SWISS-PROT:P00533"
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Pred. No. 3e-07;
); Mismatches (
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Reiter,
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Biochemistry
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nilarity 100.0%;
Conservative (
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1452. 1456
/gene="EGFR"
/note="5" splice donor site"
1463. 1569
1537. .1542
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317. .1
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SIQWRDIVSSDFLSNMSMDFQNHLGSCQKCDPSCPNGSCWGAGEENCQKLTKIICAQQ
CSGRCRGKSPSDCCHNQCAAGCTGPRESDCLKCRKFRDEATCKDTCPPLMLYNPTTYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"epidermal growth factor receptor precursor"
/protein_id="AAC50802.1"
/protein_id="AAC50802.1"
/db_xref="GI:1628550"
/tanslation="MRPSGTAGAALLALLAALCPASRALEEKKVCQGTSNKLTQLGTF
/translation="MRPSGTAGAALLALLALLAALCPASRALEEKKVCQGTSNKLTQLGTF
EDHFLSLQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mayo Clinic, 200 First St. SW, Rochester, MN 55905, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               830.
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245. .1462
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1325. 1333
/gene="EGFR"
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1298. .1306
/gene-"EGFR"
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767. .775
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KVCNG1G1GEFKDSLS1NATNIKHFKNCTSISGDLHILPVAFRGDSFTHTPPLDPQEL
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/db_xref="taxon:9606"
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Pred. No. 2.8e-07;
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BASE COUNT
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Ilekis,J.V., Gariti,J., Niederberger C. and Scoccia,B.
Expression of a Truncated Epidermal Growth Factor Receptor-like
Protein (TEGFR) in ovarian Cancer
Gyn. Onc. 65 (1997) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Epidermal growth factor receptor-like gene product and Patent: US 5708156-A 1 13-JAN-1998;
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                                                                                                                                                              Direct Submission
Submitted (25-MAR-1997) Obstetrics & Gynecology, University
Illinois at Chicago, 820 S. Wood Street, Chicago, IL 60612,
please also see Ilekis, J. in RK Miller, HA Thiede (eds):
'Molecular Biology and Cell Regulation of the Placenta.' Nev
Plenum, 103-117, 1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSU95089 1868 bp mRNA PRI 20-AFK-1997 Human truncated epidermal growth factor receptor-like protein precursor mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1868)
Ilekis, J.V., Stark, B
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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554 c 494 g
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/note="TEGFR; the calculated molecular weight of the nascent protein is approximately 42 kD (includes signal peptide at amino acid positions 1-24); the molecular
                                                  /tissue_type="placenta"
504. .575
504. .1721
                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                          A draft entry and printed copy of this sequence were kindly provided by G.Merlino (07-OCT-1985).
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2643)

Merilno,G.T., Ishii,S., Whang-Peng,J., Knutsen,T., Xu,Y.-H., Clark,A.J.L., Stratton,R.H., Wilson,R.K., Ma,D.-P.P., Roe,B.A., Hunts,J.H., Shimizu,N. and Pastan,I.

Structure and localization of genes encoding aberrant and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMEGERS 2643 bp mrNA PRI 07-NOV-1994
Human aberrant (short) epidermal growth factor receptor mRNA.
                                                                                                                                                                                                                                                                                                                      MO1. Cell. Biol. 5 (7), 1722-1734 (1985) 85267689
                                                                                                                                                                                                                                                                                                                                                                                   epidermal growth factor receptor RNAs from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human epidermoid carcinoma cell line A431, cDNA to mRNA, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epidermal growth factor; epidermal growth factor receptor; erbB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K03193.1 GI:181984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 100.0%;
Similarity 100.0%;
72; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="truncated epidermal growth factor receptor-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mrpSgtagaallallaalcpasraleekkvcqgtsnkltqlgtf
EDHFL5LQrmfnncevvlgnleltyvQrnyDlsflktqtqevagyvLtalntveriple
NLQIIRGnmfyrensyAlavLSavdaanutglkelpmrnlog:Llhgavprsnnpalcnve
SIQWRDIVSSDFLSNMSHDFQNHLGSCQKCDpSGCPGLAGEENCOKLTKIICAQQ
CSGRCRKSPSDCCHNQCAAGCTGPRESDCLVCRKFRDEATCKDTCPPLMLYRGTTYQ
MDVNPERKYSPSDCHNQCAAGCTGPRESDCLVCRKFRDEATCKDTCPPLMLYRGTTYQ
MDVNPERKYSPSDCHNQCAAGCTGPRESDCLYCRKFRDEATCKDTCPPLMLYRGTTYQ
KVCNGIGIGEFKDSLSINATNIKHFKNCTSISGDLHILPVAFRGDSFTHTPPLDPQEL
DILKTVKEITGLS"
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                                         /gene="EGFR"
160. .2133
                                                                                                                                                    /organism-"Homo sapiens"
/db_xref="taxon:9606"
/map-"7p13-p12"
<1..>2643
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/db_xref="GI:2051985"
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                                                                                    /note="EGFR(S) mRNA; G00-120-610"
). .2643
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'note-"aberrant epidermal growth factor receptor"
                    'gene="EGFR"
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Pred. No.
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Best Local
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220 GCGAGTCGGGCT 231
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704 a 693 c 699 g 547 t
Chromosome 7; 493 bp upstream of RsaI site
                                                                                                                                                                                                                                                                Clinic,
                                                                                                                                                                                                                                                                                                                  Reiter, J.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reiter,J.L., Threadgill,D.W., Eley,G.D., Strunk,K.E., Danielsen,A.J., Schehl Sinclair,C., Pearsall,R.S., Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2864)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens truncated epidermal growth factor receptor precursor
                                                                                                                                                                                                                                                                                   Submitted (01-FEB-1999) Biochemistry and Molecular Biology, Mayo
                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 71 (1), 1-20 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Comparative genomic sequence analysis and isolation of human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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CSGCRCKSPSDCCLNQCAAGCTGPRESDCLVGKKE RDEATCKDTCPPLMLYNPTTYQ
MDVNDEGKYSFGATCVKCPRNVEVTDHGSCVPACACADS YEMEBOGVRKCKCKCBCCR
KVCNGIGIGEFKDSLSINATNIKHEKNCTSISGDLHILPVAFRGDSFTHTPPLDPQEL
DILKTYKELTGFLLIQAAPENTTDLHAFENLEIIRGENTKOHGQFEAAVVSLNITSLGL
RSLKEISDGDVIISGNKNLCYANTINMKKLFGTSGQKTKIISNRGENSCKATGQVCHA
LCSPBCGWGFEPRDCVSCRNVSRGRECVDKCNLLEGBPREFVENSECIQCHPECLPQA
MNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVMGENNTLVWKYADAGHVCHLCHPNC
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/protein_id="AAA52371.1"
/protein_id="AAA52371.1"
/db_xref="GI:IB1985"
/translation="MRPSGTAGAALLALLAALCPASRALEEKKVCQGTSNKLTQLGTF
EDHFLSLQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLE
RUQIIRGNNYYENSYALAVLSNYDANKTGLKELPMRNLQEILHGAVRFSNNPALCNVE
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/gene="EGFR"
246. .2363
                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                              00 First St. SW, Rochester,
Location/Qualifiers
                                                    /tissue_type="placenta"
l. .2864
                                                                                                         /map="7p11.2-p12"
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pred. No. 2.4e-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pearsall, R.S., Green, P.J.,
                                                                                                                                                                                                                                                                MN 55905, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2643;
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Length 3633; Indels

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61 gcgagtcgggct 72
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                                                                                                                                                                                                                                                                                                                                                                                        GCGAGTCGGGCT 317
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                                    1 (bases 1 to 3633)
Pippig,S.D. and Veres,G.
Selectable cell surface marker genes
Patent: WO 0136659-A 1 25-MAY-2001;
Docation/Qualifiers
1. 3633
                                                                                                                                                                                                                                                  AX179384 3633 bp DNA
Sequence 1 from Patent WO0136659.
AX179384
                                                                                                                                                                            unidentified
                                                                                                                                                                                             unidentified
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                                                                                                                                                         unclassified
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2832. )937
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Edhflislomminkevulgnleityvognydlsflktiqlgelydarvtlalkvverfiple
nlqiirgnwyyensyalaylsnydanktglkelpmrnloeiihgavrfsnnpalcnve
siomrdiyssofisnmshofonilgscokcopscproscokcageekcokkirkiicaoq
csgrcrgkspsdcchnqcaagctgpresdclvcrkfrdeatckdtcpplhllynptyvq
mdvnpegkysfgatcykkcprnyvytdhgscyracgadsyemeedgyrkckkcegopcr
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2864
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DILKTVKEITGFLLIQAMPENRTDLHAFENLEIIRGFKROHGGFSLAVVSINTTSIGL
RSLKEISDGDVIISGNKULCVANTINMKLIFGTSGXTKIISNRGENSCKATRGOVCHA
LCSPBGCWGPEPROCVSCRNVSKGRECVDKCMLLEGEPREFVENSECIQCHPECLPQA
MNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVMGENNTLVMKYADAGHVCHLCHPNC
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WGGCSHLHAWPSASVIITASSCH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id~"AAG43240.1"
/db_xref~"GI:12002212"
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829 c
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/note="ERBB1; alternative transcript encoding only the
/organism="unidentified"
/db_xref="taxon:32644"
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SOURCE
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ACCESSION
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HUMEGFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Draft entry and computer-readable sequence for [Unpublished (1990)] kindly submitted by J.D.Haley, 12-SEP-1990.
Oncogene Science Inc.
350 Community Drive Manhasset, NY 11030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hum. Mol. Genet. 1 (2), 135 (1992)
93244774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Two chromosome 7 dinucleotide repeat polymorphisms at gene loci epidermal growth factor receptor (EGFR) and pro alpha 2 (1) collagen (COL1A2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contributory effects of de novo transcription and premature transcript termination in the regulation of human epidermal factor receptor proto-oncogene RNA synthesis J. Blol. Chem. 266 (3), 1746-1753 (1991) 91107677
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Haley, J. D. and Waterfield, M. D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell surface receptor; epidermal growth factor Human DNA, clone LIII.
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1007 c 953 g 7
    /number=1
a 1219 c
                                        /gene="EGFR"
/note="G00-120-610"
                                                                                                                                   /product="epidermal growth factor receptor"
/protein_id="AAA63171.1"
/db_xref="GI:553271"
                                                                                                                                                                                             /codon_start=1
/db_xref="GDB:G00-120-610"
                                                                                                                                                                                                                                                                                                                              /map="7p13-p12"
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/clone="LIII"
                                                                            /partial
                                                                                                                /translation~"MRPSGTAGAALLALLAALCPASRALEEKK"
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BASE COUNT ORIGIN

polyA_site polyA_site polyA_site polyA_site polyA_signal polyA_signa mat_peptide sig_peptide

receptor.

growth .

06-MAR-1995

Query Match Best Local :

Local

Matches

REFERENCE AUTHORS TITLE

FEATURES

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KEYWORDS SOURCE

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                                                                                                                                                                                                                                                                                                                  49 Convent Dr., Tel: 3014020201
Fax: 3014024735
                                                                                                                                                                                                                                                                                                                                GDB_DSEG: EGER
CONTRACT: EFIC D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08,
Tel: 3014020201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3888)

Bouffard,G.G., Iyer,L.M., Idol,J.R., Braden,V.V., Cunningham,A.F., Weintraub,L.A., Mohr Tidwell,R.M., Peluso,D.C., Fulton,R.S., Leckle,M.P. and Green,E.D.

A collection of 1814 human chromosome 7-specific STSs Genome Res. 7 (1), 59-64 (1997)
                                                                                                                                                                                                                                                   STS size: 11
PCR Profile:
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Unpublished (1997)
Synonyms: EGFR
GDB: GDB:196214
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                                                                                                                                                                Protocol
                                                                                                                                                                                                                                                                                Primer B: TTCTTCTGCACACTTGGCAC
                                                                                                                                                                                                                                                                                           Email: egreen@nhgri.nih.gov
Primer A: GTTTGAAGAATTTGAGCCAACC
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                                MgCl2:
KCl:
Tris-HCl:
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Annealing:
                      NH4C1:
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Total Vol:
                                                                                                                           dNTPs:
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PCR Cycles:
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es 72; Conserv
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King C.Richter, Kraus, M.H. and Aaronson, S.A.
erbB-2 gene segments, probes, recombinant DNA and kits for
detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This 578 has been incorporated into the NHGRI chromosome 7 physical map, but was developed by another investigator. See GenBank record: M38425 For additional information about the NHGRI chromosome 7 mapping project, see http://www.nhgri.nih.gov/DIR/GTB/CHR7. Also see Genomics 11:548-64 (1991) [MUID-92128937].
                                                                                                                                                                                                                                                                                                                                                                             Unknown
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Sequence 3 from patent US 5985553.
AR086089
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                                                                                                                                                                                                                                                                                                                                                                Unclassified.
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/gene="EGFR"
2338. .2359
/gene="EGFR"
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1 1219 c 1101
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1 1484 c 1337 g
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/db_xref="taxon:9606"
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Pred. No. 1.8e-07;
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Ullrich,A., Coussens,L., Hayflick,J.S., Dull,T.J., Gray,A.,
Tam,A.W., Lee,J., Yarden,Y., Libermann,T.A., Schlessinger,
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Mammalla; Euthería; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
187, .258
/note="Asn-linked glycosylation site" 1838. .1846
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568. .576
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RTPLLSSLSATSNNSTVACIDRNGLQSCPIKEDSFLQRYSSDPTGALTEDSIDDTFLP
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/translation="mrPSGTAGAALLALLAALCPASRALEEKKVCQGTSNKLTQLGTF
EDHFLSLQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLE
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1506. .1514
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1267. .1275
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/protein_id="CAA25240.1"
/db_xref="GI:757924"
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Waterston,R.H.
Direct Submission
Submitted (05-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
4 (bases 1 to 177998)
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Waterston, R.H.
Direct Submission
Submitted (28-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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3313. .3321
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1924. .3732
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Submitted (30-SEP-2000) Department of Genetics, Washington University, 4444 Porest Park Avenue, St. Louis, Missouri 6.
On Sep 28, 1999 this sequence version replaced gi:4662682.
Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                   The clone sequenced to the left is RP4-791C19, 200 bp overlap. Actual start of this clone is at base position 80354 of RP4-791C19; actual end is at base position 177998 of RP5-1091E12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE INFORMATION:
This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpec.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from the companion of the companion of the library is from the companion of the library is from the library is from the library is from the library in the library is from the library in the library is from the library in the library in the library is from the library in the library in the library is from the library in the library in the library is from the library in the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           one male donor.
The clowe may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send
mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEIGHBORING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
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                             /rpt_family~"L1"
2566. .2617
/rpt_family="Alu"
2744. .3029
                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
/map="7p11.2-p21"
/clone="RP5-1091E12"
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   /rpt_family="Alu"
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13289
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/note="similar to EST AI263609 (NID:g3871812) qq89g02.xl"
9298. .9472
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/note-"match to EST AI935313 (NID:g5674183) wpl6g07.x1"
9258. .9472
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9010. .9102
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4729. .5555
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4417. .4726
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4303. .439
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3138. .3497
                                                                                                 /rpt_family~"(TA)n"
18838. .18872
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11173, .13567
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15231. .15735
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13475. .13
/rpt_family="Alu"
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                                                                                                                                                                                                  note="match to EST AA640700 (NID:g2565950) nr22f01.rl"
                                                                                                                                                                                                                                                              note="match to EST A1870800 (NID:g5544768) w169a08.x1"
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/note="similar to EST R35665 (NID:g792566) yh90f01.s1"
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                                                                                                                                                                                                                                                                                                                                                                                                                  ullrich, A., Coussens, L., Hayflick, J.S., Dull, T.J., Gray, A. Tam, A. W., Lee, J., Yarden, Y., Libermann, T.A., Schlessinger, Downward, J., Mayes, E.L.V., Whittle, N., Waterfield, M.D. and Seeburg, P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF288738 197496 bp DNA PRI 26-JAN-2001
Homo sapiens epidermal growth factor receptor (EGFR) gene, complete
cds, alternatively spliced; and 5S ribosomal RNA gene, complete
Dases 9385 to 146950)
3 (bases 9385 to 146950)
Reiter, J.L. and Maihle, N.J.
A 1.8 kb alternative transcript from the human epidermal growth factor receptor gene encodes a truncated form of the receptor Nucleic Acids Res. 24 (20), 4050-4056 (1996)
                                                                                                                                                                                  Merlino,G.T., Ishii,S., Whang-Peng,J., Knutsen,T., Xu,Y.-H., Clark,A.J.L., Stratton,R.H., Wilson,R.K., Ma,D.P., Roe,B.A., Hunts,J.H., Shimizu,N. and Pastan,I. Structure and localization of genes encoding aberrant and normal epidermal growth factor receptor RNAs from A431 human carcinoma
                                                                                                                                                                                                                                                                                                                                            Human epidermal growth factor receptor cDNA sequence and aberrant expression of the amplified gene in A431 epidermoid carcinoma cells Nature 309 (5967), 418-425 (1984)
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1 (bases 9385 to 197496)
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                                                                                                                                                                                                                                                                                                      (bases 9385 to 163007)
                                                                                                                                           Cell. Biol. 5 (7), 1722-1734 (1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="MER1_type" 27828. .27915
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24327. .24359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match to EST A1694220 (NID:g4971560) wd57g01.x1" 23573. .23653
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27748. .27851
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24646. .24871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 (bases 192735 to 195366)
Eley,G., Frederick,L., Wang,X.Y., Smith,D.I. and James,C.D.
3'end structure and rearrangements of EGFR in glioblastomas
Genes Chromosomes Cancer 23 (3), 248-254 (1998)
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6 (base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reiter, J.L. and Eley, G.D. Direct Submission
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complement(4729, .5555)
/rpt_family="L1"
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/chromosome="7"
       /db_xref="db5T5:G31681"

join(9219. .9472,132393. .132544,133412. .133595,

136713. 136647,141401. .141469,142653. .142771,

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144118. .144259,145937. .146053,146640. .146756,

146866. .148239,147770. .147860,150246. .150445,

151606. .151738,153840. .153930,155387. .155544,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_type=dispersed 4084. .4302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3586, .4083)
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                                                                                                                                             8627. .12178
/note="swss1476"
                                                                                                                                                                                         /note≖"CpG Island"
                                                                                                                                                                                                                                                                                                                             /rpt_family="MSTD"
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join(9219. 9472, 32393. 132544, 133412. 133595,

136713. 136847, 141401. 141469, 142653. 142771,

144118. 144259, 145937. 146053, 146640. 146766,

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/161282. .161320,162953. .163007)
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join(9219. 9472,132393. 132544,133412. 133595.

136713. 136847,141401. .141469,142653. 142771.

144118. 144259,14593. 146053,146640. 146756.

144818. 144259,145937. 147860,150246. 150445.

161606. 151738,153840. 153930,155387. 155544,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    160414. .161152)

/genew "EGFR"

/notew "3 the alternative transcript"

/product "p110 epidermal growth factor receptor"

/evidence experimental
/protein_id="AAG35788.1"
/db_xref="GI:11494379"
                                                                 /evidence-experimental
/product_"A431-specific pl15 epidermal growth factor
                                                                                                                                                                           /gene="EGFR"
                                                                                                                                                                                                                                                                                                                                                                                  /note-"ERBB1; HER1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"truncated epidermal growth factor receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene-"EGFR"
/note-"2.4 kb alternative transcript"
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/product="p60 epidermal growth factor receptor"
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join(9219. 9472,132393. 132544,133412. 133595,
136713. 138647,141401. 141469,142653. 142771,
144118. 144259,145937. 146053,146640. 146766,
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                                                                                                                          /codon_start-1
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9219. .9384
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/note="5.8 kb transcript"
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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Rattus norvegicus egfr gene, partial cds
AB025197
                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (19-MAR-1999) to the DDBJ/EMBL/GenBank databases. Shinae R. Kondoh, Kyoto Univ. Graduate School of Medicine, Dept. of Molecular Oncology: Yoshida-Konoe-cho, Sakyo-ku, Kyoto 606-8501, Japan (E-mail:skondoh@virusl.virus.kyoto-u.ac.jp, Tel:81-75-751-4152, Fax:81-75-751-4159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kondoh, S. K. and Akiyama, N.
Rat EGFR promoter from NRK cells
Published Only in DataBase (1999) In press
2 (bases I to 1858)
Kondoh, S. K. and Akiyama, N.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus cell_line:NRK DNA.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB025197.1 GI:4586455
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   ρ
                                                                                                                                                                                                        /gene="egfr"
1775. .>1858
                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/cell_lne="NRK"
1775. .1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158630. .158636)
/gene="EGFR"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(9385. .9472,132393. .132544,133412. .133595,
136713. .136847,141401. .141459,142553. .142771.
144118. .144259,145937. .146053,146640. .146766,
146866. .145939,147770. .147860,150246. .150445,
151606. .151738,153840. .153930,155387. .155544,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mrpsgtagaallallaalcpasraleekkvcogtsnkltqloty
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siqmrdivssdelsnmsmdfqnhlgscorddecphuschkageercqkltkiicaqq
csgrcrgkspsdcchuqcaagcgrpredclycrkerdeatckdcpplhlyndtyp
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510 c 471 g 453 t
                                                      /product="egfr"
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LCSPEGCWGPEPRDCVSCRNVSRGRECVDKCNLLEGEPREFVENSECIQCHPECLPQA
MNITCTGRGPDNOIQCAYYIDGPHCVKTCPAGVMGENNTLVWKYADAGHVCHLGHPNC
                                                                                                                                                     1775. .>1858
/gene="egfr"
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                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 72; DB 9;
Pred. No. 5.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 197496;
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ORIGIN

Query Match 60.8%; Score 43.8; DB 10; Length 1858; Best Local Similarity 76.1%; Pred. No. 0.57; Matches 54; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

DЬ

Qy 61 gcgagtcgggc 71

₽ 1835 GCAGGTGGGGC 1845

Search completed: January 14, 2002, 20:13:57 Job time: 4182 sec

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   number of hits satisfying chosen parameters:
N_Geneseq_1101:*

/SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       930621 seqs, 428662619 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search time 159.75 Seconds (without alignments) 386.400 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Nucleotide sequenc	AAA58471	21	58857	40.6	29.2	c 11	
EGF receptor relat	AAC84211	22	1958	60.8	43.8	10	
pRLD1D2D3.ApaL con	AAQ43812	14	6274	83.3	60	9	
pRLD2D3D4 construc	AAQ43813	14	6207	83.3	60	8	
pRLD3D4 construct.	AAQ43814	14	5750	100.0	72	7	
Human EGF receptor	AAZ23954	21	5532	100.0	72	σ	
cDNA sequence enco	AAC61552	21	3818	100.0	72	U	
Nucleotide sequenc	AAF85332	22	3633	100.0	72	4	
Epidermal growth f	AAV06408	19	1868	100.0	72	ω	
Human epidermal gr	AAS01680	22	1663	100.0	72	N	
Human cytokine rec	AAA11949	21	1200	100.0	72	4	
Description	ID	1	Query Match Length DB	Query Match	Score	Result No.	-
				de			
	SUMMARIES						

Human colon cancer	AAH33653	22	1075	36.7	26.4	45		
Human prostacyclin	AAT05324	16	792	36.7	9	44		
HSV-2 strain SB5 C	AAV62176	19	117213	36.9	9	43	c	
Nucleotide sequenc	AAA14651	21	77536	36.9	6	42	o	
Human ORFX ORF1376	AAC75821	21	1877	36.9	26.6	41		
Candida antartica	AAV28875	19	1029	36.9	9	40		
Zea mays cinnamyl	AAX03728	20	713	37.2		39	O	
Maize cinnamoyl Co	AAV46425	19	713	37.2	6	38	C	
Mouse programmed c	AAV04449	18	844	37.5	27	37		
DNA encoding angio	AAA50532	21	782	37.5	27	36		
	AAA50497	21	782	37.5	27	υ 5		
Human W10 protein	AAA90932	21	782	37.5	27	34		
Truncated p27/p16	AAX26234	20	782	37.5	27	ω ω		
colon canc	AAH34426	22	652	37.5	27	32		
Mouse programmed c	AAV04448	18	279	37.5	27	31		
polynucle	AAI64000	22	7582	37.8	27.2	30		
HSV-2 immediate ea	AAA09686	22	3957	38.1	27.4	29		
Mycobacterium sp.	AAV49510	19	1260	38.1	27.4	28	c	
Mycobacterium tube	AAV49625	19	1260	38.1	27.4	27	ဂ	
Mycobacterium tube	AAV49626	19	1245	36.1		26	ဂ	
HSV-2 strain SB5 C	AAV62138	19	980	38.1	27.4	25	c	
Nucleotide sequenc	AAA58471	21	58857	38.6	•	24		
Zea mays DNA fragm	AAC44552	21	1879	38.6	•	23		
Sequence of beta-1	AAQ22957	13	2697	38.9	28	22		
Human epidermal gr	AAQ70935	15	54	38.9	28	21	C	
Human secreted pro	AAD13350	22	02	39.2	•	20		
Transcriptional re	AAX15110	20	5143	39.4	•	19	a	
Human CDK-inhibito	AAZ20131	20	5143	39.4	•	18	ი	
Pseudomonas alcali	AAF30870	22	17612	39.7		17	C	
Pseudomonas alcali	AAA13905	21	17612	39.7	•	16	c	
Pseudomonas Xpc, O	AAV23494	19	17612	39.7	٠	15	ი	
Mouse IRS-2 cDNA.	AAT28293	17	4088	39.7		14		
alcal	AAA13900	21	390	39.7	28.6	13	o	
Pseudomonas XcpV s	AAV23486	19	390	39.7	•	12	C	

ALIGNMENTS

RESULT AAA11949 Human cytokine receptor gene fragment DNA #2 01-AUG-2000 AAA11949; AAA11949 standard; DNA; 1200 بر (first entry)

Cytokine receptor; cell proliferative disease; diagnosis; primer; cytosine methylation; psoriasis; chronic rheumatoid arthritis; arteriosclerosis; blood vessel re-narrowing; diabetic retinopathy; premature neonate retinopathy; tumor; ss.

Homo sapiens.

W0200017339-A1

30-MAR-2000.

17-SEP-1999; 99WO-JP05069

18-SEP-1998; 98JP-0265089

(KYOW) KYOWA HAKKO KOGYO KK

Нопита У, Oyama N, Sato K;

WPI; 2000-283572/24

blood for genomic DNA extraction Rapid and highly reproducible diagnosis of cell proliferative diseases e.g. chronic rheumatoid arthritis and psoriasis, using particularly blood for genomic DNA extraction -

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RESULT
AAS01680
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tches
                                                                                                                                                                                                                                                                                                                                                                                                            Human; T-type calcium channel; CACNAIG; cytosine methylation; CpG island; cellular proliferative disorder; colorectal cancer; age related disease; apolipoprotein B; APOB; caudal type homeobox transcription factor 2; CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBM1; G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B'; HSPA6; RasGAP-related protein; IGGAP2; proteinase-activated receptor 2; PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL; patched A; patched B; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4; chromosome 7p12; ds.
The present sequence for epidermal growth factor receptor (EGFR)
                               Claim 32; Fig 4B; 125pp; English.
                                                                New nucleic acid molecule for use as a marker for screening cancer, comprises the coding region for a T-type calcium channel and regulatory sequences associated with the channel
                                                                                                                                                                                                                                                                           14-SEP-2000; 2000WO-US25479
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel rapid and highly reproducible method for diagnosis of a cell proliferative disease, comprising analyzing the extent of methylation of cytosine residue in a region participating in the chromosome DNA-related expression of a cytokine receptor gene. The method is used for the diagnosis for psoriasis, chronic rheumatoid arthritis, arteriosclerosis, blood vestely re-nearrowing, diabetic retinopathy, premature neonate retinopathy or solid tumor using body fluids or tissues, particularly blood for genomic DNA extraction. This sequence represents fragment of the human cytokine receptor described in
                                                                                                                                                                                                         (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                             15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human epidermal growth factor receptor (EGFR) CpG island.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS01680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS01680 standard; DNA; 1663 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1174 gcgagtcgggct 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                      WPI; 2001-244777/25.
                                                                                                                                                                                                                                                                                                                                               WO200119845-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1200 BP; 195 A; 430 C; 354 G; 213 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 atgegaceeteegggaceggeggegegeteetggegetgetggegeteetgeeeg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 27-28; 31pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                             99US-0398522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 72;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CpG island is used to study the methylation state of EGFR which maps to chromosome 7p12. The methylation state of specific regions within CpG islands associated with a novel T-type calcium channel CACNAIG gene correlate with several cancerous phenotypes involving various tissue and cell types. Since aberrant methylation of normally unmethylated CpG islands is often observed in immortalised and transformed cells. CACNAIG is implicated in cellular proliferative disorders e.g. leukaemia, colorectal, lung, breast and other cancers. The nucleic acid coding for CACNAIG is useful as a marker for screening cancer and age related diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for amplification of a CpG-containing nucleic acid, where the primer hypridises with a target polynucleotide sequence (AAS01677-AAS01676), can be used for detecting aberrant methylation. The CpG island sequences analysis and containing primers approached the containing primers are contained to the containing primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AASO1677-AASO1692) are selected from genes encoding CACNAIG, apolipoprotein B (APOB), caudal type homeobox transcription factor 2 (CDX2), epidermal growth factor receptor (EGFR), fibrilin-1 (FBN1), G protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B'; HSPA6), RasGAP-related protein (IGGAP2), klotho (KL), proteinase-activated receptor 2 (PAR2), paired-like homeodomain transcription factor 2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1; SDC4) or a MINT31 sequence.
                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                         Epidermal growth factor receptor-like protein; diagnosis; cancer; hyperproliferative disease;
              (ILEK/) ILEKIS J V.
                                                 31-MAY-1996;
                                                                                                                    13-JAN-1998
                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                        sig_peptide
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV06408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV06408 standard; DNA; 1868 BP
                                                                                                                                                   US5708156-A
                                                                                                                                                                                                                                                                                                                                                                                                                                               Epidermal growth factor receptor-like protein (TEGFR) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1663 BP; 199 A; 684 C; 543 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     606 gcgagtcgggct 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 gcgagtcgggct 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative (
                                               96US-0658883.
                                                                                  96us-0658883.
                                                                                                                                                                                            /*tag* b
/note* "putative signal peptide"
576..1718
                                                                                                                                                                                                                                                        /product= TEGER 504..575
                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 72; DB 22;
Pred. No. 7.4e-10;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                               TEGFR; human; antibody ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.
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   XEXTXEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This cDNA encodes a novel human epidermal growth factor receptor-like protein termed TEGFR. TEGFR is derived from human placenta. Fragments of the TEGFR cDNA can be used as a probe in a hybridisation assay to detect full length of TEGFR. An antibody can be produced using the antigen comprising at least the unique C-terminal sequence of the TEGFR polypeptide, optionally conjugated to an immunogenic carrier. The polypeptide, optionally conjugated to an immunogenic carrier. The hybridisation assay and immunoassay to detect the polypeptide. The hybridisation assay and immunoassay can be used in the diagnosis of human cancers. Antibodies and other inhibitors of the TEGFR polypeptide may also be used to treat hyperproliferative diseases including cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Columns 11-16; 17pp; English.
                                                                        19-NOV-1999; 99US-0166594
19-NOV-1999; 99US-0444038
30-MAR-2000; 2000US-0539248
                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                             Epidermal growth factor receptor 1; EGFR1; cell surface marker; protein-tyrosine kinase receptor; PTKR; immunoselection; gene ther; bone marrow transplant; graft facilitation; immune reconstitution;
                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of wild type EGFR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1868 BP; 449 A; 554 C; 494 G; 371 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide related to epidermal growth factor receptor -corresponding DNA and antibody useful for cancer diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-100411/09.
P-PSDB; AAW33737.
Pippig SD,
                           (NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN
                                                                                                                                                                   25-MAY-2001.
                                                                                                                                                                                                WO200136659-A2
                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF85332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF85332 standard; DNA; 3633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ilekis
                                                                                                                                      17-NOV-2000; 2000WO-EP11474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504 atgcgaccotocgggacygcoggggcagcgctcctggcgctgctggctgcgctctgcccg 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 atgcgaccctccgggacggccggggcagcgctcctggcgctgctgctgctgcccg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
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   Veres G
                                                                                                                                                                                                                          /transl_except= "(pos: 1618..1620, aa: Asn)"
/product= "EGFR1"
                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                VERW
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 19;
. 7.4e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1868;
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                                                                                                                                                                                                                                                                                                                                                therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT
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AAC61552
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Best Local Similarity 100.0%;
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                                                07-JUN-1995;
01-JUN-1990;
08-SEP-1989;
11-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      any nerve growth factor receptor(s) (NGFR). The method uses mutated PTKR as a cell surface marker, and is useful for identifying genetically modified cells, especially immunoselection of transduced mammalian cells, and for identifying mammalian cells expressing a protein of interest. The genetically modified marked cells may be used in an autologous or allogeneic setting e.g. gene therapy for bone marrow transplants, graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a human epidermal growth factor receptor 1 (EGFR1). EGFR is a protein-tyrosine kinase receptor (PTKR). The specification describes a method for identifying genetically modified mammalian cells. The method uses a mutated PTKR nucleic acid which comprises a modification to the intracellular and extracellular domains, or comprises a modification to the intracellular domain and excludes a modification to the intracellular domain and excludes the comprises a modification to the intracellular domain and excludes a modification to the intracellular domain and excludes the comprises a modification to the intracellular domain and excludes the comprises a modification to the intracellular domain and excludes the comprise of the comprise 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glioma; brain; breast tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA sequence encoding an epidermal growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC61552
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P-PSDB; AAB68420.
                                                                                                                                                                                   09-MAR-1999;
                                                                                                                                                                                                                                    03-OCT-2000
                                                                                                                                                                                                                                                                                          US6127126-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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(UYDU-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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DUKE
                                                                       95US-0479808.
90US-0531410.
89US-0404226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; epidermal growth factor receptor; \mathtt{EGFR}; mutant; \mathtt{lumour}; \mathtt{ss}.
                                                                                                                                                                                 99US-0264723
                                                                                                                                                                                                                                                                                                                                        /*tag~ a
/product~ "epidermal growth factor receptor"
/note~ "no termination codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 187..3817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  946 A; 1007 C; 953 G; 727 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 72;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3633;
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RESULT
AAX23954
ID AAZ2
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AC AAZ2
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AC AAZ2
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AC Hume
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DT 28-J
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DE Hume
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Best Local (
                                                                           21-OCT-1987;
01-NOV-1991;
05-MAR-1986;
                                                                                                                                                                                                                                                                   Human; v-erbB; MAC117; epidermal growth factor receptor; anticancer; cytostatic; toxin; cancer; treatment; detection; mammary carcinoma; malignant; EGF receptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes a method for diagnosing glioma in a brain cell sample suspected of being cancerous. The method comprises detecting the presence of a nucleic acid encoding an epidermal growth factor receptor (BGFR) mutant protein type II. Deletions in the EGFR gene are found in many gliomas. breast tumours and lung tumours. The method is useful for diagnosing gliomas, breast tumours and lung tumours. The present sequence encodes a normal EGFR polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing glioma in brain cell sample involves determining the presence of a nucleic acid encoding an epidermal growth factor receptor mutant protein type {\tt II} -
                                                                                                                       07-JUN-1995;
                                                                                                                                                                   US5985553-A
         WPI; 2000-012777/01
                                 Aaronson SA, Kraus MH,
                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                              16-NOV-1999
                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                               Human EGF receptor DNA
                                                                                                                                                                                                                                                                                                                                      28-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                               AAZ23954 standard; DNA; 5532 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3818 BP; 972 A; 1089 C; 1012 G; 745 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 11A-F; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAB19259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bigner D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                       247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 atgcgaccctccgggacggccggggcagcgctcctggcgctgctgctgcccg 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 gcgagtcgggct 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                           91US-0786598.
86US-0836414.
                                                                                                 87US-0110791
                                                                                                                       95US-0475035
                                                                                                                                                                                                             Location/Qualifiers
187..3819
                                                                                                                                                                                       /product= "EGF receptor"
                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                               King CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 72; DB 21;
Pred. No. 7.1e-10;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3818;
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Best Local
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                               WPI; 1993-196297/24.
P-PSDB; AAR38211.
                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                    AAQ43814 standard; DNA; 5750 BP
         New epidermal growth factor receptor truncate proteins - which
                                                                                                           12-JUN-1990;
26-OCT-1990;
                                                                                                                                            12-JUN-1990;
                                                                                                                                                                   08-JUN-1993
                                                                                                                                                                                       US5218090-A.
                                                                                                                                                                                                                                                                                                                                   pRLD3D4 construct
                                                                                                                                                                                                                                                                                                                                                        20-OCT-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                AAQ43814;
                                                                                     (WARN ) WARNER LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Column 19-30; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAY50616
                                                                                                                                                                                                                                                                                                                                                                                                                                                           247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 gcgagtcgggct 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        gcgagtcgggct 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
il Similarity 100.0%;
72; Conservativo
                                                                                                           90US-0536896.
90US-0604728.
                                                                                                                                            90US-0536896.
                                                                                                                                                                                                                                 Location/Qualifiers
1077..1079
                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                              /note= "codon ARA encodes Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 72; DB 21 Pred. No. 7e-10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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This invention describes a novel purified nucleic acid (I) (v-erbB related gene) specifically hybridizing to all or part of a MAC117 gene and not hybridizing to nucleic acid encoding an epidermal growth factor receptor. The product of the invention has anticancer and cytostatic activity. Antibodies to the protein encoded by (I) are conjugated to toxins and kill cancer cells expressing (I). Antibodies to the protein encoded by (I) are useful for the treatment of cancer. Fragments of (I) and the MAC117 gene are useful as probes for the detection of human mammary carcinoma or other malignancies resulting from the v-erbB related gene. This sequence encodes a human epidermal growth factor (EGF)
Epidermal growth factor receptor truncate protein; EGF; binding sites; adsorptive agents; mammalian cell growth abnormality; detection; growth; reproduction; signal transmission; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5532 BP; 1472 A; 1484 C; 1337 G; 1239 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purified nucleic acid useful for detection and treatment of mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 atgcgaccctccgggacggccggggcagcgctcctggcgctgctgctgcgctctgcccg 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 atgogacoctcogggacoggggcagogctcotggcgctgctgctgctgctctgcccg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 5532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
AAQ43813
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5750 BP; 1367 A; 1479 C; 1536 G;
                                                                                                                                                                                                                                                                                                        binding sites; adsorptive agents; mammalian cell grow detection; growth; reproduction; signal transmission;
                                                                                                                                                                                                                                                                                                                      Epidermal growth factor receptor truncate protein; EGF; binding sites; adsorptive agents; mammalian cell growth
                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                              pRLD2D3D4 construct
                                                                                                                                                                                                                                                                                                                                                                                          20-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ43813;
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ43813 standard;
                                     12-JUN-1990;
26-OCT-1990;
                                                                                                        08-JUN-1993
                                                                                                                                  US5218090-A
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            (WARN ) WARNER LAMBERT CO
                                                                              12-JUN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 gcgagtcgggct 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ligands of EGF receptor without transmitting signal for growth
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                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                       90US-0536896
90US-0604728
                                                                               90US-0536896
                                                                                                                                                                                    /*tag= a
/codon= 707-708 (
/note= "encodes I
1519..1521
                                                                                                                                                                                                                                         Location/Qualifiers 665..2193
                                                                                                                                                                       /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
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                                                                                                                                                            "codon ARA encodes Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                6207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
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Pred. No. 7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                     CG encodes Ile
LD2D3D4 *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5750;
                                                                                                                                                                                                                                                                                                                       growth abnormality;
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RESULT
AAQ43812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New epidermal growth factor receptor truncate proteins - which bind ligands of EGF receptor without transmitting signal for growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-196297/24.
P-PSDB; AAR38210.
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                                                                                                                                                                                                                                                                                      Epidermal growth factor receptor truncate protein; EGF; growth; binding sites; adsorptive agents; mammalian cell growth abnormality; detection; reproduction; signal transmission; pRLDID2D3ApaL; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ43812 standard; DNA; 6274 BP
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                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                            pRLD1D2D3.ApaL construct.
                                                                                                                                                                                                                                                                                                                                                                                               20-OCT-1993
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                                08-JUN-1993
                                                                US5218090-A
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                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                     1939.,1941
                                                                                                                                                   /codon= 707-708 CG encodes Ile
/note= "encodes LD1D2D3ApaL"
                                                                                                                                                                                                       665..2253
                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                  note= "codon ARA encodes Ile
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98.6%;
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Pred. No. 6.6e-07;
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12-JUN-1990;

90US-0536896

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AAC84211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local :
                                                                               CDS
                                                                                                       Key
5'UTR
                                      3'UTR
                                                                                                                                                 Homo sapiens
                                                                                                                                                                        Epidermal growth factor receptor; EGF receptor related protein; EGFR; ERRP; cell proliferation; colon cancer; antitumour; ss.
                                                                                                                                                                                                                EGF receptor related protein (ERRP) encoding cDNA.
                                                                                                                                                                                                                                               19-MAR-2001
                                                                                                                                                                                                                                                                            AAC84211;
                                                                                                                                                                                                                                                                                                     AAC84211 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6274 BP; 1506 A; 1610 C; 1664 G; 1493 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 3; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New epidermal growth factor receptor truncate proteins - which bind ligands of EGF receptor without transmitting signal for growth
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26-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                        724 gcgagtcgggct 735
                                                                                                                                                                                                                                                                                                                                                                                                                       665 atgcgaccctccgggacggccggggcagcgctcctggcgctgc-ggctgcgctctgcccg 723
                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
hes 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      gcgagtcgggct 72
                                                                                                                                                                                                                                               (first entry)
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90US-0604728.
                                  /*tag= b
/product= 1665..1955
                                                                        /*tag- a
228..1664
                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                     cDNA;
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                                                                                                                                                                                                                                                                                                     1958
                                                "ERRP"
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Pred. No.
                                                                                                                                                                                                                                                                                                     ВР
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. 6.5e-07;
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RESULT 11
AAA58471/c
ID AAA584
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Best Local S
Matches 54
 CDS
                                 CDS
                                                                                                                                                         Streptomyces verticillus
                                                                                                                                                                                         BLM gene cluster; bleomycin gene cluster; polyketide metabolite; bleomycin; bleomycin analogue; holo-carrier protein; thiazolidin
                                                                                                                                                                             thiazoline; bithiazoline; microbial metabolite; sugar; ss.
                                                                                                                                                                                                                       Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30.
                                                                                                                                                                                                                                                 31-OCT-2000
                                                                                                                                                                                                                                                                       AAA58471;
                                                                                                                                                                                                                                                                                            AAA58471 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This DNA encodes an epidermal growth factor (EGF) receptor related protein (ERRP). The ERRP is highly homologous to the mouse EGFR and a truncated rat EGFR. The ERRP can be expressed by standard recombinant methodology. The ERRP acts as a EGFR receptor modulator. The ERRP cDN when transfected into colon cancer cell line is useful for inhibiting proliferation of the cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-025007/03.
P-PSDB; AAB48033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1958 BP; 514 A; 524 C; 478 G; 442 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 30-31; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel epidermal growth factor receptor related protein and polynucleotide useful for inhibiting proliferation of cancer cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Majumdar A;
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                                                                                                                                                                                                                                                                                                                                                                                         atgogaccotcagggaccgcgagaaccacactgctggtgctgctgaccgcgctctgcgcg 287
                                                                                                                                                                                                                                                                                                                                               gcaggtggggc 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US12884.
                              /transl_except=
/note= "ORF 29;
2767..3486
/*tag= c
/note* "ORF
3527..5593
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                                                                            561..2309
                                                                                      /transl_except=
/note= "ORF 30;
                                                                                                                         223..564
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                                                                  /*tag≖
                                                                                                                                  ocation/Qualifiers
                                                                                                              *tag•
                                                                                                                                                                                                                                                                                           DNA; 58857
                                                                                                                                                                                                                                                                                                                                                                                                                                                60.8%;
76.1%;
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           28;
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Pred. No. 0
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                                           (pos: 1.
encodes
          encodes AAB07558
                                                                                       (pos: 1..3, aa: Met)
encodes AAB07556"
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0.0071;
                                           ..3, aa: Met)
AAB07557"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                        thiazolidine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1958;
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               WO200040704-A1
                                            /transl_except=
/note= "ORF 9; e)
57583..58857
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/note= "ORF 27;
5806..12294
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/note= "ORF 19;
37299..39215
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47178..49985
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/note= "ORF 20;
35818..37302
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32893..34830
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/note= "ORF 24;
21010..24666
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/transl_except=
/note= "ORF 15;
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/note= "ORF 23;
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12291..15491
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/note= "ORF 18;
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/note= "ORF 14;
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/note= "ORF 16;
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/note= "ORF 10;
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/note= "ORF 12;
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1..56093
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                              encodes AAB07578"
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encodes AAB07577"
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encodes AAB07570"
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encodes AAB07568"
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AAB07559*
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AAB07563"
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                                                                                  ..3, aa: Met)
AAB07576"
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AAB07572"
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13-JUL-2000

(GEMV) GENENCOR INT INC

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RRESULT 12
AAV234
AX AAV234
AC AAV234
AX AS PSeudo
XX Kinase
KW Sigma
XX Si
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Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10786 GGACGGCGGCGCCCCCCCCCCCCGCGATGACGGCGGCGAGGCGCTCGTCGGGCTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JAN-1999;
05-FEB-1999;
05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents the BLM (Bleomycin) gene cluster, containing open reading frames (ORFs) 8-30. The proteins encoded by the gene cluster are useful for producing peptides and/or polyketide metabolites, especially bleomycin or bleomycin analogues. They are also useful for chemically modifying biological molecules to produce branched methyl groups, and for coupling amino acids and fatty acids. They may be reacted with an apo-carrier protein and coenzyme A to produce a holo-carrier protein. The BLM gene cluster or catalytic domains can be used individually or collectively to produce thiazoline, thiazoline, bithiazoline and bithiazoline-containing microbial metabolites. The BLM gene cluster may also be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAB07556, AAB07557, AAB07558, AAB07559, AAB07560, AAB07561, AAB07562, AAB07563, AAB07564, AAB07565, AAB07567, AAB07568, AAB07569, AAB07571, AAB07572, AAB07573, AAB07573, AAB07576, AAB07576, AAB07576, AAB075776, AAB07578.
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                                                                                                                                                                                                                                                                                                      Kinase; LipQ; LipR; lipase expression regulator; DNA binding regulator; sigma 54 promoter; secretion factor; lux-box binding element; orfV-box binding element; regulation cascade; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas XcpV secretion
                                                                                                                                                                                                         WO9806836-A2
                                                                                                                                                                                                                                                       Pseudomonas alcaligenes
                                                     16-AUG-1996;
                                                                                                       15-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58857
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99US-0118848.
2000US-0477962.
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                                                       96US-0699092
                                                                                                       97WO-US14450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7256 A;
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Pred.
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RESULT 13
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Expression vector for producing heterologous proteins in host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes the XcpV secretion factor of Pseudomonas alcaligenes. The DNA represents a nucleic acid of the invention. The nucleic acids encode: (a) a kinase from a Pseudomonad that regulates the expression of a lipase; (b) a DNA binding regulator from a Pseudomonad that regulates the expression of a lipase; (c) a Pseudomonas alcaligenes upstream activating sequence; (d) a P. alcaligenes sigma 54 promoter that regulates the expression of a lipase; (e) a P. alcaligenes secretion factor selected from XcpP, Q, R, S, T, U, Y, W, X, Y and Z, and OrfV, X, Y; (f) a P. alcaligenes lux-box binding element; and (g) a orfV-box binding element. The nucleic acids represent parts of a regulation cascade, comprising at its heart a kinase and a DNA binding regulator. These sequences can be used for the production of heterologous proteins in a host cell. The cascade also comprises secretion factors which can
                                                                                                                                                                                                                              11-APR-2000
                                                                                                                                                                                                                                                                                                                                           Pseudomonas alcaligenes; expression; lipase regulation cascade; kinase; DNA binding regulator; polymerase; promoter; secretion factor; XcpP; XcpQ; XcpR; XcpS; XcpT; XcpU; XcpV; XcpW; XcpX; XcpX; XcpZ; XcpZ; OrfV; OrfX; OrfX; OrfZ; LipO; LipR; upstream activating sequence;
                                        P-PSDB; AAY82597
                                                        WPI; 2000-316896/27
                                                                                          Gerritse G,
                                                                                                                                                             16-AUG-1996;
                                                                                                                                                                                            15-AUG-1997;
                                                                                                                                                                                                                                                                US6048710-A
                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas alcaligenes XcpV nucleotide sequence SEQ ID NO:20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA13900 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding proteins involved in the lipase regulation cascade from P. alcaligenes - useful for controlling production essertion of heterologous proteins in P. alcaligenes
                                                                                                                         (GEMV ) GENENCOR INT INC
                                                                                                                                                                                                                                                                                               Pseudomonas alcaligenes
                                                                                                                                                                                                                                                                                                                               detergent; cleaning formulation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 390 BP; 57 A; 127 C; 154 G; 52 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enhance the secretion of produced proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 37; 106pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 TGCCACAGCCAGCGCCGCGCGTAGCTCTCCTCGCCCTCGCGGGGCCCTCGCCCGG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                          Quax WJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                           96US-0699092
                                                                                                                                                                                            97US-0911853
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Pred. No. 44;
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RESULT 14
AAT28293
ID AAT282
XPXA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an expression vector comprising a nucleic acid encoding a kinase and a DNA binding regulator which hybridises under stringent conditions to a nucleic acid isolated from pseudomonas alcaligenes. Also described are: (1) an isolated comprising the above expression vector; (2) a method of transforming a host cell comprising adding the above plasmid to host cells under appropriate conditions; (3) a transformed host cell comprising the above expression vector; and (4) a method for producing a protein comprising the steps of obtaining a host cell comprising the above expression vector; and (4) a method for producing a protein, and culturing the host cell under conditions for the expression vector and further comprising nucleic acid encoding the protein, and culturing the host cell under conditions for the expression of protein. The expression vector of the present invention can be used for producing heterologous proteins in host cells, particularly, lipase in Pseudomonas. Lipases produced can be used in detergents and cleaning formulations in Industrial processes. The invention provides a higher production level and efficiently express a heterologous protein. The present sequence encodes XcpV isolated from Pseudomonas alcaligenes, from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                          CDS
                                                 P-PSDB; AAR96994
                                                               WPI; 1996-209351/21.
                                                                                                                                (JOSL-) JOSLIN DIABETES CENT INC
(USSH) US DEPT HEALTH & HUMAN S
                                                                                                                                                                                    03-OCT-1994;
                                                                                                                                                                                                                     03-OCT-1995;
                                                                                                                                                                                                                                                       11-APR-1996
                                                                                                                                                                                                                                                                                      W09610629-A1
                                                                                                                                                                                                                                                                                                                                                                                           Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT28293 standard; cDNA; 4088 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse IRS-2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises a nucleic acid encoding a kinase and a DNA binding regulator which hybridizes under stringent conditions to nucleic acid \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                         IRS-2; insulin receptor substrate-2; diabetes; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 TGCCACAGCCAGCGCGCGCGCGTAGCTCTCCTCGCCCTGCTCGCGGCCCTCGCCCGG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 tgcgaccctccgggacggccggggcagcgctcctggcgctgctgctgctgctctgcccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Fig 3; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                                                                                                                                                                                                         vector; antibody; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 57 A; 127 C; 154 G; 52 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                    94US-0317310
                                                                                                                                                                                                                   95WO-US13041.
                                                                                               χJ,
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 60..4025
                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28.6;
Pred. No. 44;
                                                                                                                                    SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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New insulin receptor substrate polypeptide and corresp. nucleic rectors, antibodies etc., useful for diagnosis, treatment and

acid

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RESULT 15
AAV23494/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A partial cDNA sequence (AAT28293) codes for mouse insulin receptor substrate-2, or IRS-2 (AAR06994), a substrate for the insulin receptor, interleukin-4 receptor and interleukin-15 receptor. The cDNA clone was isolated from a mouse lung cDNA library by screening with clones from other libraries obtd. using probe 60 (see AAT28294-95). The open reading frame shows 51% identity to the IRS-1 sequence. IRS-2 expression was detected in heart, brain, spleen, lung, liver, skeletal muscle, kidney, testis and FDC-P2 cells. The cDNA can be used for prodn. of recombinant IRS-2 or as a probe e.g. transgene can be used to study insulin-related disorders, e.g. type II diabetes. IRS-2 genes may also be used in gene
                                                                                                                                                                                                                                                                                                                                                             Kinase; LipQ; LipR; lipase expression regulator; DNA binding regulator; sigma 54 promoter; secretion factor; lux-box binding element; orfV-box binding element; regulation cascade; ss.
           CDS
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                                              CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV23494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV23494 standard; DNA; 17612 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4088 BP; 810 A; 1400 C; 1187 G; 691 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           assessing risk of diabetes etc., also for drug screening
                                                                                                                                                                                                                                                                                                                                     Pseudomonas alcaligenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 47-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
         /*tag= h
/product= XcpT
13282..13806
                                                                                                                                                                                                                            complement (4151..3510)
                                                                                                                                                                                                                                                               complement (3513..1564)
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/*tag= f
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12853..13275
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72.5%;
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Pred. No. 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4088;
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Search completed: January 14, Job time: 4318 sec

Db 14050 TGCCACAGCCAGCGCCCGGCGTAGCTCTCCTCGCCCTGCTCGCGGGCCCTCGCCCGG 13992

0;

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Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                           This sequence encodes the Orfy, Orfy, Orfx, and Xpc secretion factors of pseudomonas alcaligenes. The DNA represents a nucleic acid of the invention. The nucleic acids encode: (a) a kinase from a Pseudomonad that regulates the expression of a lipase; (b) a DNA binding regulator from a pseudomonad that regulates the expression of a lipase; (c) a Pseudomonas alcaligenes upstream activating sequence; (d) a P. alcaligenes signa 54 promoter that regulates the expression of a lipase; (e) a P. alcaligenes secretion factor selected from Xcpp, Q, R, S, T, U, V, W, X, Y and Z, and Orfv, X, Y; (f) a P. alcaligenes liav-box binding element; and (g) a regulation cascade, comprising at its heart a kinase and a DNA binding regulator. These sequences can be used for the production of heterologous proteins in a host cell. The cascade also comprises secretion factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-1998
                                                                                                       Sequence 17612 BP; 2698 A; 6026 C; 6039 G; 2836 T; 13 other;
                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 43-48; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                    secretion of heterologous proteins in P. alcaligenes
                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding proteins involved in the lipase regulation cascade from P. alcaligenes - useful for controlling production and
                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEMV ) GENENCOR INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09806836-A2
                                                                                                                                  which can enhance the secretion of produced proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-159528/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-1996;
AAW99999
                                      Conservative
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14869..15822
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14189..14872
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16961..17473
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                                   score 28.6; D
Pred. No. 38;
0; Mismatches
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                                      19;
                                                               Length 17612;
                                      Indels
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                                      Gaps
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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                  Score
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Copyright (c) 1993 - 2000 Comp
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AU099322 AU099322
BE327106 hw07b09.x
BF056131 7j88g05.x
BF058287 7k29all.x
                AW170373 xn60e06.x
AI858079 wj70b02.x
AW163375 au94d11.y
AW163038 au91e07.y
AI554567 tn25f08.x
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        A1935313
       tn25f08.x
wp16g07.x
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	BF316964	AZ848888	BF624156	BF485106	BG605564	BF066019	AL142056	AV434418	BE421073	BE413373	AL503950	BF255166	BE471264	BE453010	AL552108	BE704513	BF903827	BE362171	, вғ660321	AK014017	AK004944	AK004883	_	w	\sim	_	v	~	~		AQ938957	AI263609	AI740805
	601903917	2M0150P06	HVSMEa001	WHE1793_E	WHE2239_D	HV_CEb001	Anopheles	AV434418	HWM005.E0	MCG011.H0	AL503950	HVSME£000	WHE0286_B	894067E09	AL552108	Sc01_08d0	MR1-MT028	DG1_84_F1	maa29d03.	Mus	Mus mus	Mus	Mus muscu	602073728	602023406	602887822	ul20al1.y	190f01.s	UI-H-BW1-	43g09.	5	19g02.	90

ALIGNMENTS

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
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AW138053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                           source
                                                                                                                                                                                                                          Seq prime POLYA=No.
                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B.

Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
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UI-H-BII-abw-c-07-0-UI.SI NCI_CGAP_Sub3
IMAGE:2713332 3', mRNA sequence.
AW138053 AW138053.1 GI:6142371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 243)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                              primer: M13
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IndeE:271332"
/clone_lib="NCI_CGAP_Sub3"
/lab_host="PHIOB (Life Technologies)"
/lab_host="PHIOB (Life Technologies)"
/note="Vector: pTy3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The
                                                                                                                                                                        Location/Qualifiers
1. .243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens cDNA clone
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wg66b11

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DEFINITION
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Best Local :
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                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 300)

Suzukl,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

In silico mapping of the 5'-ends of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries constructed by
Contact: Yutaka Suzuki
                                                      Oligo-capping method 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 bp mRNA EST 05-APR-2001 AU099322 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone HRC09161 similar to Human mRNA for precursor of epidermal growth factor receptor, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU099322,1 GI:13550451
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Pred. No. 1.6e-07;
); Mismatches 0;
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BASE COUNT

Matches

ACCESSION VERSION KEYWORDS SOURCE

AU099322

REFERENCE

AUTHORS

ORGANISM

TITLE

COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukidims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                               info@image.llnl.gov
possible reversed clone: polyT not found
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: Capabs 'email.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE327106.1 GI:9200882
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/note-*Organ: lung: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction.
                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3182201"
/clone_lib="NCI_CGAP_Lu24"
                                                                                                                     /tissue_type="carcinoid"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 1.6e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 475)
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                                                                                                                                                                                                                                          /note="Organ: pooled; Vector: pT7T3D-Fac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3393560"
/clone=lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                                  libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares NbHF pool 1: 309384-310919, 323208-325895 Soares NbZHP pool 1: 145032-14535, 15002 - 150407, 151176-152327 Soares NbZHFB-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-30311, 320136-32283, 325280-32663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento
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Pred. No. 1.6e-07;
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Query Match Best Local Similarity

Score 72; Pred. No.

DB 11; 1.6e-07;

Length 475;

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VERSION
KEYWORDS
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Best Local :
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215 GCGAGTCGGGCT 226
                                                                            155 ATGCGACCCTCCGGGACGGCCGGGGCAGCGCTCCTGGCGCTGCTGCCGCGCTCTGCCCG 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-femail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael .
R. Emmert-Fuck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72;
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                                                                                                                                                       . Similarity
72; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                info@image.linl.gov
Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia; Eutheria: Primates: Catarrhini: Hominidae: Homo. 1 (bases 1 to 476) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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                                                                                                                                                                                                                                                                        96 a
                                                                                                                                                                                                                                                                                                      double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was
                                                                                                                                                                                                                                                                                                                                                                                        constructed by Bento Soares and M. Fatima Bonaldo.
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/clone_lib="NCI_CGAP_Ov18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
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                                                                                                                                                       Score 72; DB 11;
Pred. No. 1.6e-07;
; Mismatches 0;
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                                                                                                             A1858079 582 bp mRNA EST 21-DEC-1999 wj70b02.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408139 3's similar to gb:K03193 EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mil.nlh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 561)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                      Homo sapiens
                                                                                 (HUMAN);, mRNA sequence.
AI858079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW170373.1 GI:6401898
EST.
                                                      EST
                                                                    AI858079.1 GI:5511695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Possible reversed clone: polyT not found Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                           148
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                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organisme"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2698114"
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                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 72; DB 10; 100.0%; Pred. No. 1.6e-07;
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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nes 72; Conserv
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                                                                                                                                                                                                                                                                                                            AW163375 645 bp mRNA EST 09-NOV-1999 au94d11.yl Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783925 5' similar to 9b:K03193 EPIDERWAL GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 645)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing V: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llni.gov/bbrp/lmage/image.html
Insert Length: 1510 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
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1 (bases 1 to 582)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/nclcgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                             EST
                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-*Organ: lung: Vector: pr/rsu-rac virus-modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differentiated (4 pooled tumors, including primary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMANGE:2408139"
/clone_lib="NCI_CGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH108 (phage-resistant)"
/note="Organ: lung: Vector: pT773D-Pac (Pharmacla) with a
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                                                            AUTHORS
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Other_ESTs: au94d11.x1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 646)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                        AW163038 646 bp mRNA EST 09-NOV-1999 au91e07.yl Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783652 5' similar to gb:K03193 EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
                                                                                                                                                                                        AW163038.1 GI:6302071
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                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: brain; Vector: pBluescript SK (Stratagene); Site_1: SstI; Site_2: XhOI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="5 months post-conception"
/lab_host="DH10B"
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/clone="IMAGE:2783925"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Schneider fetal brain 00004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="frontal lobe"
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                                                          AUTHORS
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              Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.

1 (bases 1 to 678)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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Contact: Wilson RK
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Unpublished (1997)
                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                     (HUMAN);, mRNA sequence.
AI554567
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Location/Qualifiers
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Seq primer: -40RP from Gibco
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Unpublished (1998)
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                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/dev_stage="5 months post-conception"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Schneider fetal brain 00004"
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                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs -r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                               Unpublished (1997)
                                                                                                                Tumor Gene Index
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 757)
                                                                                                                                                                                                               Homo sapiens
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DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2168679"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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206 GCGAGTCGGGCT 217
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                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                       Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1042 Std Error: 0.00
Seq primer: -40UP from Gibco
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Insert Length: 1220 Std Error: 0.00
Seq primer: -400p from Gibco
High quality sequence stop: 446.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 798)
                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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                                                                                                                 quality sequence stop: 468.
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/lab_host="DH10B (phage-resistant)"

/lab_host="DH10B (phage-resistant)"

/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco R1 adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco R1 sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

171 a 211 c 214 g 154 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:2465052"
/Clone_lib="NCI_CGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                           Location/Qualifiers
1. .798
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 72; DB 10;
Pred. No. 1.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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DEFINITION
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                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI740805 805 bp mRNA EST 19-DEC-1999 wg24d08.xl Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clore IMAGE:23660313 similar to gb:K03193 EPIDERMAL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 805)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 1250
                                                                                                                                                                                                                                                                                                                                                                                                           THAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                 guality sequence stop: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares wbHSF pool 1: 309384-310919, 323208-325895 Soares wbHSF pool 1: 145032-147335, 147720-148103, 148872-149255, 15002-150407, 151176-152327 Soares wbHSF-9W pool 1: 758280-760583, 772104-774407 Soares wbHSFA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares whHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:2370045"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soares and M. Fatima Bonaldo."
215 c 221 g 167 t
                                                   /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
Following HAP purification,
                                                                                                                                                          /clone="IMAGE:2366031"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                      /lab_host="DH10B"
  ibraries were mixed, and ss circles were made in vitro. Ollowing HAP purification, this DNA was used as tracer
                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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Pred. No. 1.6e-07;
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RESULT 1 AI740805

COCUS

SOURCE KEYWORDS VERSION ACCESSION

FEATURES

COMMENT

JOURNAL

AUTHORS TITLE

RENCE

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128

Matches

Ş В

61

188

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RESULT 1
AI263609
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    BASE COUNT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI263609 502 bp mRNA EST U3-FEB-1999 902.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clor iMAGE:1938578 3' similar to gb:K03193 EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 502)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trace considered overall poor quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 1254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 33308-325895 Soares NbHPP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2HFP-9W pool 1: 758280-7560583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322823, 336280-325663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento
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(Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pY773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 137 c 139 g 117 t 1 others
                                                                                                                               Soares and M. Fatima Bonaldo."
227 c 222 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the same 5 libraries. The pools consisted of the following
                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:1938578"
/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH108"
                                                                                                             Double-stranded cDNA was ligated to Eco RI adaptors
                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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Pred. No.
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, 1.6e-07;
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Search completed: January 14, 2002, 19:36:02 Job time: 1957 sec
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AUTHORS
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ORGANISM
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AQ938957
LOCUS
UNITION
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VERSION
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                                                                                                                                                                                                       Query Match 78.9%; Score 56.8; DB 13; Length 340; Best Local Similarity 94.5%; Pred. No. 0.00046; Matches 69; Conservative 0; Mismatches 3; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 84.2%;
Best Local Similarity 94:0%;
Matches 63; Conservative
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                                                                                                                                          214 GGCNAGTCGGGCT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 GTGAGTC 191
                                                                                                  60 ggcgagtcgggct 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Podowski RM
Center for Genomics Research
Karolinska Institute
17177 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-37983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 340)
1 (bases 1 to 340)
2abarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovska,V.V., Xie, Li, J., Muravenko,O.V., Kozyrev,S., Petrenko,L., Skobeleva,N., Li,J., Protopopov,A., Rashuba,V., Ernberg,I., Winberg,G. and Wahlestedt,C.
NotI clones in the analysis of the human genome
Nucleic Acids Res. 28 (7), 1635-1639 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ938957 340 bp DNA GSS 23-AUG-2000 NL1-DO11C Human NotI clones Homo sapiens genomic, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          Class: NotI site.
                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Raf.Podowski@cgr.ki.se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ938957.1 GI:7215335 GSS.
                                                                                                                                                                                                                                                                                                             51 a
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60.6; DB 10; Length 502;
Pred. No. 6.2e-05;
0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                           4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                           Gaps
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